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OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 06:47:30 : Search time 91 Seconds
(without alignments)
2411.878 Million cell updates/sec

Title: US-10-059-152-1
Perfect score: 555
Sequence: 1 gagtataataagtaacaa.....cgcgtcgtactgacgcgcgc 555

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 355320 seqs, 197730502 residues

Total number of hits satisfying chosen parameters: 710640

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:
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13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	59.8	5756	9	US-09-548-880-1
2	256	46.1	1767	10	US-09-886-942-19
3	256	46.1	4207	10	US-09-887-006-4
4	256	46.1	4210	10	US-09-897-006-5
5	256	46.1	4665	10	US-09-759-960-7
6	256	46.1	4864	10	US-09-812-133-5
7	256	46.1	5713	9	US-09-966-976A-5
8	256	46.1	5713	10	US-09-963-206B-5
9	256	46.1	6219	9	US-09-966-976A-4
10	256	46.1	6219	10	US-09-963-206B-4
11	256	46.1	6255	10	US-09-897-006-13
12	256	46.1	6827	10	US-09-982-610-17
13	256	46.1	6978	10	US-09-872-733-15
14	256	46.1	6984	9	US-10-001-189-45
15	256	46.1	7160	8	US-08-786-531B-5
16	256	46.1	7235	8	US-08-786-531B-6
17	256	46.1	7352	8	US-08-786-531B-4
18	256	46.1	7353	8	US-08-786-531B-1
19	256	46.1	7607	10	US-09-982-610-19

20	256	46.1	8282	9	US-09-966-976A-7	Sequence 7, Appl1
21	256	46.1	8282	10	US-09-963-206B-7	Sequence 7, Appl1
22	256	46.1	8345	9	US-09-966-976A-8	Sequence 8, Appl1
23	256	46.1	8345	10	US-09-963-206B-8	Sequence 8, Appl1
24	256	46.1	8366	10	US-09-872-733-6	Sequence 6, Appl1
25	256	46.1	9108	10	US-09-882-610-45	Sequence 45, Appl1
26	256	46.1	9511	10	US-09-897-006-34	Sequence 34, Appl1
27	254.4	45.8	750	10	US-09-965-697-3	Sequence 25, Appl1
28	254.4	45.8	996	8	US-08-900-220C-25	Sequence 25, Appl1
29	254.4	45.8	996	10	US-09-151-999-25	Sequence 25, Appl1
30	254.4	45.8	1104	10	US-09-845-899A-6	Sequence 6, Appl1
31	254.4	45.8	1689	10	US-09-886-942-9	Sequence 9, Appl1
32	254.4	45.8	1758	10	US-09-886-942-2	Sequence 2, Appl1
33	254.4	45.8	1767	10	US-09-886-942-8	Sequence 8, Appl1
34	254.4	45.8	1767	10	US-09-886-942-15	Sequence 15, Appl1
35	254.4	45.8	1767	10	US-09-886-942-21	Sequence 21, Appl1
36	254.4	45.8	1813	10	US-09-794-975-8	Sequence 8, Appl1
37	254.4	45.8	2947	10	US-09-798-675-2	Sequence 2, Appl1
38	254.4	45.8	3570	10	US-09-881-457A-1	Sequence 1, Appl1
39	254.4	45.8	4622	10	US-09-924-231-6	Sequence 6, Appl1
40	254.4	45.8	5070	10	US-09-795-005A-41	Sequence 41, Appl1
41	254.4	45.8	5432	10	US-09-794-975-9	Sequence 9, Appl1
42	254.4	45.8	5446	10	US-09-844-645-3	Sequence 3, Appl1
43	254.4	45.8	5458	10	US-09-912-436-11	Sequence 11, Appl1
44	254.4	45.8	5458	10	US-09-912-436-12	Sequence 12, Appl1
45	254.4	45.8	5614	10	US-09-912-436-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-548-880-1
Sequence 1, Application US/09548880
Patent No. US20020160507A1
GENERAL INFORMATION:
APPLICANT: No. US20020160507A1, Robert
TITLE OF INVENTION: Multiple Host Expression Vector
FILE REFERENCE: 700399.90118
CURRENT APPLICATION NUMBER: US/09/548, 880
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 5756
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Expression
US-09-548-880-1
Query Match 59.8%; Score 332; DB 9; Length 5756;
Best Local Similarity 74.6%; Pred. No. 8.5e-67;
Matches 543; Conservative 0; Mismatches 10; Indels 175; Gaps 3;
2 ACTATTATATAGTAATCAATTCACGGGCTCATTAGTTCATAGCCCATATATGAGATGCCG 61
834 ACTATTATATAGTAATCAATTCACGGGCTCATTAGTTCATAGCCCATATATGAGATGCCG 893
62 GTTACATATACGTAATGCGCCCGCCGCTACCGCCCAAGACCCCGCCCATG 121
894 GTTACATATACGTAATGCGCCCGCCGCTACCGCCCAAGACCCCGCCCATG 953
122 AGCTAATATAGCATATGTTCCCATATAGACCAATAGGACCTTCATTGACGTCAA 181
954 AGCTAATATAGCATATGTTCCCATATAGACCAATAGGACCTTCATTGACGTCAA 1013
182 TGGGTGAGTATTTAGGTAACGTAACGTAACGTAACGTAACGTAACGTAACGTAACGTAAC 240
1014 TGGGTGAGTATTTAGGTAACGTAACGTAACGTAACGTAACGTAACGTAACGTAACGTAAC 1073

OY	241	AGTAGGCCCCCTATTGACGCAATGACGGGAAATG-----	276
Db	1074	AGTAGGCCCCCTATTGACGCAATGACGGGAAATG-----	1133
OY	277	-----	276
Db	1134	ATGACCTTATGGACTTTCCTACTGTGGCAGTACCTACGTATAGTCAATGCTATTAC	1193
OY	277	-----	276
Db	1194	ATGCATGTCAGAGTGAGCCCAAGTTCGTCTCACTCCCAATCTCCCCCTCC	1253
OY	277	-----ATGCAGTATTTTGTGCAGCGATGAGGGC-----Gg 306	
Db	1254	ACCCCCAATTTTGTATTATTATTATTTTAAATTTTGTGACGATGGGGCGGGGG	1313
OY	307	GGGGGGGGGGCGCCCGCCAGCGGGGGCGGGCGGAGGGCGGGGGCGGCGAGCG	366
Db	1314	GGGGGGGGGGCGCCCGCCAGCGGGGGCGGGCGGAGGGCGGGGGCGGCGAGCG	1373
OY	367	GAGAGGTGCGCGCGGCACGCAATCAGAGCGGGCGGTCCGCAAGTTCTTTTATGCGAG	426
Db	1374	GAGAGGTGCGCGCGGCACGCAATCAGAGCGGGCGGTCCGCAAGTTCTTTTATGCGAG	1433
OY	427	GCGCGCGCGGGCGGCCCTATATAAAGCGAAGCGCGCGCGGGCGGGAGTGTGTCGCG	486
Db	1434	GCGCGCGCGGGCGGCCCTATATAAAGCGAAGCGCGCGGGCGGGAGTGTGTCGCG	1493
OY	487	CTGCGCTTGCGCCCGTGCCCGGCTCGCGCGCGGCTCTGCGCGCGCGCGCGCGCTGTGACT	546
Db	1494	CTGCGCTTGCGCCCGTGCCCGGCTCGCGCGCGGCTCTGCGCGCGCGCGCGCGCTGTGACT	1553
OY	547	GACGCGGT 554	
Db	1554	GACGCGGT 1561	

RESULT 2
 US-09-886-942-19
 Sequence 19, Application US/09886942
 Patent No. US20020081708A1
 GENERAL INFORMATION:
 APPLICANT: PUNNONEN, JUHA
 WRIGHT, ANNE
 SEMONOV, ANDREY
 APPLICANT:
 TITLE OF INVENTION: NOVEL CHIMERIC PROMOTERS
 FILE REFERENCE: 02-031910US
 CURRENT APPLICATION NUMBER: US/09/886,942
 CURRENT FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: 60/213,829
 PRIOR FILING DATE: 2000-06-23
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 19
 LENGTH: 1767
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-886-942-19

Query Match	46.18;	Score 256;	DB 10;	Length 1767;
Best Local Similarity	97.88;	Pred. No. 1.2e-49;		
Matches 270;	Conservative 0;	Mismatches 5;	Indels 1;	Gaps 1

QY	2	AGTTTAAATAGTATCAATTAACGGGGCATTAATCTTACAGCCCATATATGAGATTCCGC	61
Db	229	AGTTAATAATAGTATCAATTAACGGGGCATTAATCTTACAGCCCATATATGAGATTCCGC	288
QY	62	GTTAATAACTTAAGCTAAATTTGGCCCGGGCGTACCGCCCAAGACCCCGGCCATTG	121
Db	289	TTTAAATATACCTTAACGTAATAATGGCCCGCTGCTGACCGCCCAAGACCCCGGCCATTG	348
QY	122	ACGTCAAATTAATGACGTATGTTCCCATAGTAAAGCCCAATATGAGACTTTCATATGACGTCAA	181

Db	349	ACGTCAATAAATGAGCTAATGTTCCCATATGTAACGCCAATAGGACCTTCCATTCAGCTCAA	408
Oy	182	TGGTGCGAGTATTACGCTAAACTGCCCC-TTGGCACTACATCAAGTGTCATATGCCA	240
Db	409	TGGGCGAGTATTACGCTAAACGCCCACTGGCACTACATCAAGTGTCATATGCCA	468
Oy	241	AGTACGCCCCCTATTGACGCTCAATGACGGTAAATGG	276
Db	469	AGTACGCCCCCTATTGACGCTCAATGACGGTAAATGG	504

RESULT 3
 US-09-897-006-4
 Sequence 4, Application US/09897006
 Patent No. US20020106729A1
 GENERAL INFORMATION:
 APPLICANT: Block, Gregory
 TITLE OF INVENTION: Expression Vectors
 FILE REFERENCE: GALA-06415
 CURRENT APPLICATION NUMBER: US/09/897,006
 CURRENT FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: 60/215,851
 PRIOR FILING DATE: 2000-07-03
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 4
 LENGTH: 4207
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-09-897-006-4

Query Match	46.18;	Score 256;	DB 10;	Length 4207;
Best Local Similarity	97.88;	Pred. No. 1.4e-49;		
Matches 270;	Conservative 0;	Mismatches 5;	Indels 1;	Gaps 1;

QY	2	AGTTATTAATGATATCAATACAGGGGTCATTATTCATACGCCATATATGAGATTCGGC	61
Db	154	ACTTATTATTAAGTAAATCAATACGGGGTCATTATTCATACGCCATATATGAGATTCGGC	213
QY	62	GTTACATAACTTACGGTAAATTTGGCCCGCGCGTCAGCCCAAGACCCCGCCCAATTG	121
Db	214	GTTACATAACTTACGGTAAATTTGGCCCGCGCGTCAGCCCAAGACCCCGCCCAATTG	273
QY	122	ACGCAATAAATGAGCTANGTCCCATAGTACGGCCAAATAGGAGATTCCATATGACGTAA	181
Db	274	ACGCAATAAATGAGCTANGTCCCATAGTACGGCCAAATAGGAGATTCCATATGACGTAA	333
QY	182	TGGGTGGAGTATTTACGGTAAACTGCCCCA-TTGGCAGTACATCAAGTATATCATATGCCA	240
Db	334	TGGGTGGAGTATTTACGGTAAACTGCCCCA-TTGGCAGTACATCAAGTATATCATATGCCA	393
QY	241	AGTACGCCCCCTATGAGCTAAATGACGGTAAATGG	276
Db	394	AGTACGCCCCCTATGAGCTAAATGACGGTAAATGG	429

RESULT 4
US-09-897-006-5
; Sequence 5, Application US/09897006
; Patent No: US20020106729A1
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1 APPLICANT: Black, Gregory
2 TITLE OF INVENTION: Expression Vectors
3 FILE REFERENCE: GALA-06415
4 CURRENT APPLICATION NUMBER: US/09/897,006
5 CURRENT FILING DATE: 2001-06-29
6 PRIOR APPLICATION NUMBER: 60/215,851
7 PRIOR FILING DATE: 2000-07-03
8 NUMBER OF SEQ ID NOS: 36
9 SOFTWARE: PatentIn version 3.0

SEQ ID NO 5
LENGTH: 4210
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-897-006-5

Query Match 46.1%; Score 256; DB 10; Length 4210;
Best Local Similarity 97.8%; Pred. No. 1.4e-49;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 AGTATTATAGTAATCAATTAACGGGGTCATAGTTCATAGCCCATATATGAGTTCGCC 61
DB 153 AGTATTATAGTAATCAATTAACGGGGTCATAGTTCATAGCCCATATATGAGTTCGCC 212
QY 62 GTTACATACTTACGTAATTAATGGCCCGGCTGACGCCCAAGACCCCGCCCATTTG 121
DB 213 GTTACATACTTACGTAATTAATGGCCCGGCTGACGCCCAAGACCCCGCCCATTTG 272
QY 122 ACCTCAATATAGCAATTAATGCTTCCCATAGTACGCTCA 181
DB 273 ACCTCAATATAGCAATTAATGCTTCCCATAGTACGCTCA 332
QY 182 TGGGTGAGTATTATGAGTAACTGCCA-TTGGCAGTACATCACTGATCATATGCCA 240
DB 333 TGGGTGAGTATTATGAGTAACTGCCA-TTGGCAGTACATCACTGATCATATGCCA 392
QY 241 AGTACGCCCCCTATTGACGTCAATGACGGTAAATGG 276
DB 393 AGTACGCCCCCTATTGACGTCAATGACGGTAAATGG 428

RESULT 5

US-09-759-960-7
Sequence 7, Application US/09759960
Patent No. US2001000639A1

GENERAL INFORMATION:

APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Collins, Edward J.
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,960
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/169,425
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/004002
TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 4665 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-759-960-7

Query Match 46.1%; Score 256; DB 10; Length 4665;
Best Local Similarity 97.8%; Pred. No. 1.4e-49;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 AGTATTATAGTAATCAATTAACGGGGTCATAGTTCATAGCCCATATATGAGTTCGCC 61
DB 2625 AGTATTATAGTAATCAATTAACGGGGTCATAGTTCATAGCCCATATATGAGTTCGCC 2684
QY 62 GTTACATACTTACGTAATTAATGGCCCGGCTGACGCCCAAGACCCCGCCCATTTG 121
DB 2685 GTTACATACTTACGTAATTAATGGCCCGGCTGACGCCCAAGACCCCGCCCATTTG 2744
QY 122 ACCTCAATATAGCAATTAATGCTTCCCATAGTACGCTCA 181
DB 2745 ACCTCAATATAGCAATTAATGCTTCCCATAGTACGCTCA 2804
QY 182 TGGGTGAGTATTATGAGTAACTGCCA-TTGGCAGTACATCACTGATCATATGCCA 240
DB 2805 TGGGTGAGTATTATGAGTAACTGCCA-TTGGCAGTACATCACTGATCATATGCCA 2864
QY 241 AGTACGCCCCCTATTGACGTCAATGACGGTAAATGG 276
DB 2865 AGTACGCCCCCTATTGACGTCAATGACGGTAAATGG 2800

RESULT 6

US-09-812-133-5
Sequence 5, Application US/09812133
Patent No. US20020065240A1

GENERAL INFORMATION:

APPLICANT: Thomas, Kenneth A., Jr.
APPLICANT: Kendall, Richard L.
APPLICANT: Bell, Andrew J.
APPLICANT: Huckle, William R.
TITLE OF INVENTION: GENE THERAPY FOR STIMULATION OF
FILE REFERENCE: 20073P
CURRENT APPLICATION NUMBER: US/09/812,133
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: PCT/US98/22668
PRIOR FILING DATE: 1998-10-23
PRIOR APPLICATION NUMBER: 60/063,629
PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 4864
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: E. coli
US-09-812-133-5

Query Match 46.1%; Score 256; DB 10; Length 4864;
Best Local Similarity 97.8%; Pred. No. 1.4e-49;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 AGTATTATAGTAATCAATTAACGGGGTCATAGTTCATAGCCCATATATGAGTTCGCC 61
DB 338 AGTATTATAGTAATCAATTAACGGGGTCATAGTTCATAGCCCATATATGAGTTCGCC 397
QY 62 GTTACATACTTACGTAATTAATGGCCCGGCTGACGCCCAAGACCCCGCCCATTTG 121
DB 398 GTTACATACTTACGTAATTAATGGCCCGGCTGACGCCCAAGACCCCGCCCATTTG 457
QY 122 ACCTCAATATAGCAATTAATGCTTCCCATAGTACGCTCA 181

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Db 458 ACGTCAATTAATGAGCTATGTTCCCATGTAACGCCCAATAGGAGCTTTCATTCAGCTCAA 517
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Qy 182 TGGGTGAGATTAATTAACGTAACAGCCCA-TTGGCAGTACATCAAGTGTATCATATGCGCA 240
|||
Db 518 TGGGTGAGATTAATTAACGTAACAGCCCACTGGCAGTACATCAAGTGTATCATATGCGCA 577
|||
Qy 241 AGTACGCCCCCTATTGACGTCATAGCGGTAATGG 276
|||
Db 578 AGTACGCCCCCTATTGACGTCATAGCGGTAATGG 613
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RESULT 7

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US-09-966-976A-5
; Sequence 5, Application US/09966976A
; Patent No. US20020168649A1
; GENERAL INFORMATION:
; APPLICANT: Ferrick, David A.
; APPLICANT: Swift, Susan E.
; APPLICANT: Armstrong, Randall
; APPLICANT: Fox, Bryan
; TITLE OF INVENTION: Secretion and Compositions for Screening for Modulators and Ige Syt
; FILE REFERENCE: A-66038-4/RMS/JUD/DLR
; CURRENT FILING DATE: 2001-09-27
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5713
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-966-976A-5
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Query Match 46.1%; Score 256; DB 9; Length 5713;
Best Local Similarity 97.8%; Pred. No. 1.4e-49;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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Qy 2 AGTATTAATAGTATCAATTAACGGGGTCATTAGTTCATACCCCATATATGAGTTCCGC 61
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Db 102 AGTATTAATAGTATCAATTAACGGGGTCATTAGTTCATACCCCATATATGAGTTCCGC 161
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Qy 62 GTTACATACCTAGCGTAATTTGGCCGCGGTGACCGCCCAAGACCCCGCCCATTTG 121
|||
Db 162 GTTACATACCTAGCGTAATTTGGCCGCGGTGACCGCCCAAGACCCCGCCCATTTG 221
|||
Qy 122 ACGTCAATTAATGAGCTATGTTCCCATGTAACGCCCAATAGGAGCTTTCATTCAGCTCAA 181
|||
Db 222 ACGTCAATTAATGAGCTATGTTCCCATGTAACGCCCAATAGGAGCTTTCATTCAGCTCAA 281
|||
Qy 182 TGGGTGAGATTAATTAACGTAACAGCCCA-TTGGCAGTACATCAAGTGTATCATATGCGCA 240
|||
Db 282 TGGGTGAGATTAATTAACGTAACAGCCCACTGGCAGTACATCAAGTGTATCATATGCGCA 341
|||
Qy 241 AGTACGCCCCCTATTGACGTCATAGCGGTAATGG 276
|||
Db 342 AGTACGCCCCCTATTGACGTCATAGCGGTAATGG 377
|||
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RESULT 8

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US-09-963-206B-5
; Sequence 5, Application US/09963206B
; Patent No. US20020123076A1
; GENERAL INFORMATION:
; APPLICANT: Ferrick, David A.
; APPLICANT: Swift, Susan E.
; APPLICANT: Armstrong, Randall
; APPLICANT: Fox, Bryan
; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige Syt
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; TITLE OF INVENTION: Secretion and Switch Rearrangement
; FILE REFERENCE: A-66038-3/RMS/JUD/DLR
; CURRENT APPLICATION NUMBER: US/09/963, 206B
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/076,624
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5713
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-963-206B-5
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Query Match 46.1%; Score 256; DB 10; Length 5713;
Best Local Similarity 97.8%; Pred. No. 1.4e-49;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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Qy 2 AGTATTAATAGTATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 61
|||
Db 102 AGTATTAATAGTATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 161
|||
Qy 62 GTTACATACCTAGCGTAATTTGGCCGCGGTGACCGCCCAAGACCCCGCCCATTTG 121
|||
Db 162 GTTACATACCTAGCGTAATTTGGCCGCGGTGACCGCCCAAGACCCCGCCCATTTG 221
|||
Qy 122 ACGTCAATTAATGAGCTATGTTCCCATGTAACGCCCAATAGGAGCTTTCATTCAGCTCAA 181
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Db 222 ACGTCAATTAATGAGCTATGTTCCCATGTAACGCCCAATAGGAGCTTTCATTCAGCTCAA 281
|||
Qy 182 TGGGTGAGATTAATTAACGTAACAGCCCA-TTGGCAGTACATCAAGTGTATCATATGCGCA 240
|||
Db 282 TGGGTGAGATTAATTAACGTAACAGCCCACTGGCAGTACATCAAGTGTATCATATGCGCA 341
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Qy 241 AGTACGCCCCCTATTGACGTCATAGCGGTAATGG 276
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Db 342 AGTACGCCCCCTATTGACGTCATAGCGGTAATGG 377
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RESULT 9

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US-09-966-976A-4
; Sequence 4, Application US/09966976A
; Patent No. US20020168649A1
; GENERAL INFORMATION:
; APPLICANT: Ferrick, David A.
; APPLICANT: Swift, Susan E.
; APPLICANT: Armstrong, Randall
; APPLICANT: Fox, Bryan
; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige
; FILE REFERENCE: A-66038-4/RMS/JUD/DLR
; CURRENT FILING DATE: 2001-09-27
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 6219
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-966-976A-4
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Query Match 46.1%; Score 256; DB 9; Length 6219;
Best Local Similarity 97.8%; Pred. No. 1.5e-49;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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Qy 2 AGTATTAATAGTATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 61
|||
```

Db 102 AGTATTATATAGTATCAATTACGGGGGTGCTATTGTTCAATGACCCCAATATATGAGTTCCGC 161
Qy 62 GTTACATTAATTAAGGTAATTTGGCCCGCGCTGACCCGCAACGACGCCGCCCATTTG 121
Db 162 GTTACATTAATTAAGGTAATTTGGCCCGCGCTGACCCGCAACGACGCCGCCCATTTG 221
Qy 122 AGTCAATTAATGACGATGTTCCCATAGTAACGCCCAATAGGAGCTTTCCATTGACGTCAA 181
Db 222 AGTCAATTAATGACGATGTTCCCATAGTAACGCCCAATAGGAGCTTTCCATTGACGTCAA 281
Qy 182 TGGGTGAGTATTTACGTTAACTGCCCA-TTGGCAGTACATCAAGTATATATATGCA 240
Db 282 TGGGTGAGTATTTACGTTAACTGCCCA-TTGGCAGTACATCAAGTATATATATGCA 341
Qy 241 AGTACGCCGCCCTATTGACGTCAATGACGTTAAATGG 276
Db 342 AGTACGCCGCCCTATTGACGTCAATGACGTTAAATGG 377

RESULT 10
US-09-963-2068-4
Sequence 4, Application US/099632068
Patent No. US20020123076A1
GENERAL INFORMATION:
APPLICANT: Ferrick, David A.
APPLICANT: Swift, Susan E.
APPLICANT: Armstrong, Randall
TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige Syn
FILE REFERENCE: A-66038-3/RMS/JJD/DLR
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 09/076,624
PRIOR FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 6219
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-963-2068-4

Query Match 46.1%; Score 256; DB 10; Length 6219;
Best Local Similarity 97.8%; Pred. No. 1.5e-49;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 2 AGTATTATATAGTATCAATTACGGGGGTGCTATTGTTCAATGACCCCAATATATGAGTTCCGC 61
Db 102 AGTATTATATAGTATCAATTACGGGGGTGCTATTGTTCAATGACCCCAATATATGAGTTCCGC 161
Qy 62 GTTACATTAATTAAGGTAATTTGGCCCGCGCTGACCCGCAACGACGCCGCCCATTTG 121
Db 162 GTTACATTAATTAAGGTAATTTGGCCCGCGCTGACCCGCAACGACGCCGCCCATTTG 221
Qy 122 AGTCAATTAATGACGATGTTCCCATAGTAACGCCCAATAGGAGCTTTCCATTGACGTCAA 181
Db 222 AGTCAATTAATGACGATGTTCCCATAGTAACGCCCAATAGGAGCTTTCCATTGACGTCAA 281
Qy 182 TGGGTGAGTATTTACGTTAACTGCCCA-TTGGCAGTACATCAAGTATATATATGCA 240
Db 282 TGGGTGAGTATTTACGTTAACTGCCCA-TTGGCAGTACATCAAGTATATATATGCA 341
Qy 241 AGTACGCCGCCCTATTGACGTCAATGACGTTAAATGG 276
Db 342 AGTACGCCGCCCTATTGACGTCAATGACGTTAAATGG 377

RESULT 11
US-09-897-006-13
Sequence 13, Application US/09897006

Patent No. US20020106729A1
GENERAL INFORMATION:
APPLICANT: Bleck, Gregory
TITLE OF INVENTION: Expression Vectors
FILE REFERENCE: GALA-06415
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,851
PRIOR FILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 6255
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-897-006-13

Query Match 46.1%; Score 256; DB 10; Length 6255;
Best Local Similarity 97.8%; Pred. No. 1.5e-49;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 2 AGTATTATATAGTATCAATTACGGGGGTGCTATTGTTCAATGACCCCAATATATGAGTTCCGC 61
Db 2805 AGTATTATATAGTATCAATTACGGGGGTGCTATTGTTCAATGACCCCAATATATGAGTTCCGC 2864
Qy 62 GTTACATTAATTAAGGTAATTTGGCCCGCGCTGACCCGCAACGACGCCGCCCATTTG 121
Db 2865 GTTACATTAATTAAGGTAATTTGGCCCGCGCTGACCCGCAACGACGCCGCCCATTTG 2924
Qy 122 AGTCAATTAATGACGATGTTCCCATAGTAACGCCCAATAGGAGCTTTCCATTGACGTCAA 181
Db 2925 AGTCAATTAATGACGATGTTCCCATAGTAACGCCCAATAGGAGCTTTCCATTGACGTCAA 2984
Qy 182 TGGGTGAGTATTTACGTTAACTGCCCA-TTGGCAGTACATCAAGTATATATATGCA 240
Db 2985 TGGGTGAGTATTTACGTTAACTGCCCA-TTGGCAGTACATCAAGTATATATATGCA 3044
Qy 241 AGTACGCCGCCCTATTGACGTCAATGACGTTAAATGG 276
Db 3045 AGTACGCCGCCCTATTGACGTCAATGACGTTAAATGG 3080

RESULT 12
US-09-982-610-17
Sequence 17, Application US/09982610
Patent No. US20020146420A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
Bennett, Brian D.
Goeddel, David
Lee, James M.
Mathews, William
Tsai, Siao Ping
Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,610
FILING DATE: 17-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/446,648

FILING DATE: 1996-MAY-23

APPLICATION NUMBER: 08/222616

FILING DATE: 04-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0821P3PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 6827 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-982-610-17

Query Match 46.1%; Score 256; DB 10; Length 6827;

Best Local Similarity 97.8%; Pred. No. 1.5e-49;

Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 AGTATTATATAGTATCATATACGGGGTCAATAGTTCATAGCCCATATATGAGTTCGCC 61

DB 31 AGTATTATATAGTATCATATACGGGGTCAATAGTTCATAGCCCATATATGAGTTCGCC 90

QY 62 GTTACATACTTACGTAATATGCGCGCGGCTGACGCCGCCACGACCCCGCCCATTTG 121

DB 91 GTTACATACTTACGTAATATGCGCGCGGCTGACGCCGCCACGACCCCGCCCATTTG 150

QY 122 ACGCAATAATGAGTATGTTCCCATAGTAACGCAATGAGGACTTTCATAGAGTCA 181

DB 151 ACGCAATAATGAGTATGTTCCCATAGTAACGCAATGAGGACTTTCATAGAGTCA 210

QY 182 TGGGTGAGTATTTACGTAATGCGCGCGGCTGACGCCGCCACGACCCCGCCCATTTG 240

DB 211 TGGGTGAGTATTTACGTAATGCGCGCGGCTGACGCCGCCACGACCCCGCCCATTTG 270

QY 241 AGRACGCCCCCTATTGACGTCAATGACGTAATG 276

DB 271 AGRACGCCCCCTATTGACGTCAATGACGTAATG 306

RESULT 13

US-09-872-733-15

Sequence 15, Application US/09872733

Patent No. US2001003655A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as

TITLE OF INVENTION: MOLECULAR CLONES WITH MODIFIED HIV GAG/POL, SIV GAG AND

FILE REFERENCE: SIV ENV GENES

CURRENT FILING DATE: 2001-06-01

PRIOR APPLICATION NUMBER: US/09/872,733

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/173,036

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 6978

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: DNA sequence

US-09-872-733-15

Query Match 46.1%; Score 256; DB 10; Length 6978;

Best Local Similarity 97.8%; Pred. No. 1.5e-49;

Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 AGTATTATATAGTATCATATACGGGGTCAATAGTTCATAGCCCATATATGAGTTCGCC 61

DB 96 AGTATTATATAGTATCATATACGGGGTCAATAGTTCATAGCCCATATATGAGTTCGCC 155

QY 62 GTTACATACTTACGTAATATGCGCGCGGCTGACGCCGCCACGACCCCGCCCATTTG 121

DB 156 GTTACATACTTACGTAATATGCGCGCGGCTGACGCCGCCACGACCCCGCCCATTTG 215

QY 122 ACGCAATAATGAGTATGTTCCCATAGTAACGCAATGAGGACTTTCATAGAGTCA 181

DB 216 ACGCAATAATGAGTATGTTCCCATAGTAACGCAATGAGGACTTTCATAGAGTCA 275

QY 182 TGGGTGAGTATTTACGTAATGCGCGCGGCTGACGCCGCCACGACCCCGCCCATTTG 240

DB 276 TGGGTGAGTATTTACGTAATGCGCGCGGCTGACGCCGCCACGACCCCGCCCATTTG 335

QY 241 AGRACGCCCCCTATTGACGTCAATGACGTAATG 276

DB 336 AGRACGCCCCCTATTGACGTCAATGACGTAATG 371

RESULT 14

US-10-001-189-45

Sequence 45, Application US/10001189

Patent No. US2002017363A1

GENERAL INFORMATION:

APPLICANT: FRASER JR., MALCOLM J.

APPLICANT: LI, XU

TITLE OF INVENTION: BEAM, TERESA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING

FILE REFERENCE: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION

CURRENT FILING DATE: 835910-92098

PRIOR APPLICATION NUMBER: US/10/001,189

PRIOR FILING DATE: 2001-10-30

PRIOR APPLICATION NUMBER: 60/244,984

PRIOR FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 60/244,677

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 45

LENGTH: 6984

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: pBXP3-DsRed-ori sequence

US-10-001-189-45

Query Match 46.1%; Score 256; DB 9; Length 6984;

Best Local Similarity 97.8%; Pred. No. 1.5e-49;

Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 AGTATTATATAGTATCATATACGGGGTCAATAGTTCATAGCCCATATATGAGTTCGCC 61

DB 2 AGTATTATATAGTATCATATACGGGGTCAATAGTTCATAGCCCATATATGAGTTCGCC 61

QY 62 GTTACATACTTACGTAATATGCGCGCGGCTGACGCCGCCACGACCCCGCCCATTTG 121

DB 62 GTTACATACTTACGTAATATGCGCGCGGCTGACGCCGCCACGACCCCGCCCATTTG 121

QY 122 ACGCAATAATGAGTATGTTCCCATAGTAACGCAATGAGGACTTTCATAGAGTCA 181

DB 122 ACGCAATAATGAGTATGTTCCCATAGTAACGCAATGAGGACTTTCATAGAGTCA 181

QY 182 TGGGTGAGTATTTACGTAATGCGCGCGGCTGACGCCGCCACGACCCCGCCCATTTG 240

DB 182 TGGGTGAGTATTTACGTAATGCGCGCGGCTGACGCCGCCACGACCCCGCCCATTTG 240

Db 182 TGGGTGAGATATTACGGTAACCTGCCACTTGGCAGTACATCAAGTATCATATGCA 241
OY 241 AGTACGCCCCCTATTGACGTCAATGAGCGTAATGG 276
Db 242 AGTACGCCCCCTATTGACGTCAATGAGCGTAATGG 277

RESULT 15

US-08-786-531B-5
; Sequence 5, Application US/08786531B
; Patent No. US20020013979A1
; GENERAL INFORMATION:
; APPLICANT: Link, Charles J.
; APPLICANT: Levy, John P.
; APPLICANT: Wang, Suming
; APPLICANT: Seregina, Tatiana
; TITLE OF INVENTION: Vehicles for Stable Transfer of Green
; TITLE OF INVENTION: Fluorescent Protein Gene and Methods of Use for Same
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zarley, McKee, Thome, Voorhees & Sease
; STREET: 801 Grand Suite 3200
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/786,531B
; FILING DATE: 21-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010371
; FILING DATE: 22-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nebel, Heidi S.
; REGISTRATION NUMBER: 37,719
; REFERENCE/DOCKET NUMBER: hgtf1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515-288-1367
; TELEFAX: 515-288-1338
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7160 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-786-531B-5

Query Match 46.18; Score 256; DB 8; Length 7160;
Best Local Similarity 97.88; Pred. No. 1.5e-49;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY 2 AGTTATTATATGATCATATACGGGGTCATTATGTCATAGCCCATATATGAGTTCCGC 61
Db 2813 AGTTATTATATGATCATATACGGGGTCATTATGTCATAGCCCATATATGAGTTCCGC 2872
OY 62 GTTACATACTTACGTAATTTGGCCCGCGCTGACCGCCCAAGACCCCGCCCATTTG 121
Db 2873 GTTACATACTTACGTAATTTGGCCCGCGCTGACCGCCCAAGACCCCGCCCATTTG 2932
OY 122 ACGTCAATATGAGCATATGTCCTCCATATGACGCCAATAGGACCTTTCATTTGACGTCAA 181
Db 2933 ACGTCAATATGAGCATATGTCCTCCATATGACGCCAATAGGACCTTTCATTTGACGTCAA 2992
OY 182 TGGGTGAGATATTACGGTAACCTGCCA-TTGGCAGTACATCAAGTATCATATGCA 240

Db 2993 TGGGTGAGATATTACGGTAACCTGCCACTTGGCAGTACATCAAGTATCATATGCA 3052
OY 241 AGTACGCCCCCTATTGACGTCAATGAGCGTAATGG 276
Db 3053 AGTACGCCCCCTATTGACGTCAATGAGCGTAATGG 3088

Search completed: December 15, 2002, 08:34:42
Job time : 107 secs

Db 563 AGTCCGCCCCCTATTGACGTCATGACGGTAATGGCCCGCCTGGCATTATGCCCAGTAC 622


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: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:PLASMID
: OTHER INFORMATION: p43rsm5CB-AT
US-09-299-141-11

Query Match          58.6%; Score 325; DB 4; Length 6924;
Best Local Similarity 74.9%; Pred. No. 8.2e-63;
Matches 543; Conservative 0; Mismatches 10; Indels 172; Gaps

OY      2  AGTTTAAATGATGATCAATTACGGGGGTCATTAGTTCATACGCCCATATATGAGATCCGC 61
      |||||||
Db       533  AGTATTAATATGTAATCAATTACGGGGTCATTAGTTCATACGCCCATATATGAGATCCGC 592

OY      62  GTTACATAACTTACAGGTAATATGGCCCCCGGCTACCGGCCCAACGACCCCCGCCCATTTG 121
      |||||||
Db       593  GTTACATAACTTACAGGTAATATGGCCCCCGGCTACCGGCCCAACGACCCCCGCCCATTTG 652

OY      122  ACGTCAATAATGACGTATGTTCCCATPAATGAACGCCAATAGGACCTTCCATTAGAGTCA 181
      |||||||
Db       653  ACGTCAATAATGACGTATGTTCCCATPAATGAACGCCAATAGGACCTTCCATTAGAGTCA 712

OY      182  TGGGAGGAGTATTTACGGTAAACTGCCCCA-TTGGCAGTACATCAAGTATCATATGCCA 240
      |||||||
Db       713  TGGGAGGAGTATTTACGGTAAACTGCCCCA-TTGGCAGTACATCAAGTATCATATGCCA 772

OY      241  AGTACGGCCCCCTAATTGACGTCAATGACGTAATATGG----- 276
      |||
Db       773  AGTACGGCCCCCTAATTGACGTCAATGACGTAATATGGCCCCCGCTGGCATTAATGCCAGTAC 832

OY      277  ----- 276
Db       833  ATGACCTTACGGGACTTCTACTTGCGCAGTACATCTACGTATTAGTCATCGCTATTAC 892

OY      277  ----- 276
Db       893  ATGTCGAGGTGAGACCCACAGCTCTGCTCACTCTCCCATCTCCCCCCCCCTCCACACC 952

OY      277  -----ATGACGATATTTTGTGCGAGGATGGGGG-----GGGGG 310
      |||
Db       953  CCAATTTTGTATTATTTATTTATTTTAAATTTATTTTGTGCGAGGATGGGGGCGGGGGGG 1012

OY      311  GGGGGGCGCGCCAGCGAGCGGGGGGGGGCGGCGAGGGGCGGGCGGCGAGCGGAGAGA 370
      |||
Db       1013  GGGGGGCGCGCCAGCGAGCGGGGGGGGGCGGCGAGGGGCGGGCGGCGAGCGGAGAGA 1072

OY      371  GGTGCGGCGGCGACGCCAATCAGAGCGGGCGGCTCCGAAAGTTTCTTTATATGCGAGGCGG 430
      |||
Db       1073  GGTGCGGCGGCGACGCCAATCAGAGCGGGCGGCTCCGAAAGTTTCTTTATATGCGAGGCGG 1132

OY      431  CGGGGGGCGGGCCCTAATAAAAGCGAAGCGCGGGCGGGGGGAGTGTGCTGGCG--CGGTG 489
      |||||||
Db       1133  CGGGGGGCGGGCCCTAATAAAAGCGAAGCGCGGGGGGGGAGTGTGCTGGCGAGCGGTG 1192

OY      490  CTTTGGCCCCCTGGCCGCTCCGCGCGGCGCTCCGCGCGCGCGCGCGCGCGGCTGTGACTGAC 549
      |||||||
Db       1193  CTTTGGCCCCGCTGGCCGCGCTCCGCGCGGCGGCGCTCCGCGCGCGCGCGCGGCTGTGACTGAC 1252

OY      550  CGCGT 554
      ||||
Db       1253  CGCGT 1257

RESULT 5
US-08-459-493-1
: Sequence 1, Application US/08459493
: Patent No. 6030638
: GENERAL INFORMATION:
: APPLICANT: Brigham, Kenneth
: APPLICANT: Conary, Jon T.
: APPLICANT: Canonico, Angelo
: APPLICANT: Meyrick, Barbara
: TITLE OF INVENTION: PLASMID FOR IN VIVO EXPRESSION

```

;; TITLE OF INVENTION: PROSTAGLANDIN SYNTHASE
;; NUMBER OF SEQUENCES: 3
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
;; STREET: 100 S. Wacker Drive - Suite 960
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: U.S.A.
;; ZIP: 60606-4002
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/459,493
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/080,221
;; FILING DATE: 21-JUNE-1993
;; APPLICATION NUMBER: US 07/746,941
;; FILING DATE: 19-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kohn, Kenneth I.
;; REGISTRATION NUMBER: 30,955
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (313) 456-8000
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 763 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: circular
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: Promoter
;; LOCATION: 1..763
;; US-08-459-493-1
;
Query Match 46.1%; Score 256; DB 3; Length 763;
Best Local Similarity 97.8%; Pred. NO. 7.7e-48;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY 2 AGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 61
DB 180 AGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 239
OY 62 GTTACATACTTACGGTAATTTGCGCGCGGTGACCGGCCAACGACCCCGCCCATG 121
DB 240 GTTACATACTTACGGTAATTTGCGCGCGGTGACCGGCCAACGACCCCGCCCATG 299
OY 122 AGCTCAATATAGCATGATGTTCCCATATAGCCCAATAGGAGCTTTCATTGAGCTCA 181
DB 300 AGCTCAATATAGCATGATGTTCCCATATAGCCCAATAGGAGCTTTCATTGAGCTCA 359
OY 182 TGGGTGAGATTTTACGTAACCTGCCCA-TTGGCAGTACATCAAGTATCATATGCA 240
DB 360 TGGGTGAGATTTTACGTAACCTGCCCACTGGCAGTACATCAAGTATCATATGCA 419
OY 241 AGTACGCCCTATTGACGTCATATGAGGTAATG 276
DB 420 AGTACGCCCTATTGACGTCATATGAGGTAATG 455

RESULT 6
US-08-029-022-2
; Sequence 2, Application US/08029022
; Patent No. 5641662
; GENERAL INFORMATION:

;; APPLICANT: Debs, Robert J.
;; APPLICANT: Zhu, Ning
;; TITLE OF INVENTION: TRANSECTION OF LUNG VIA AEROSOLIZED
;; TITLE OF INVENTION: TRANSEGENE DELIVERY
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson
;; STREET: 2200 Sand Hill Road, Suite 100
;; CITY: Menlo Park
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 94025
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
;; COMPUTER: IBM PS/2 Model 502 or 55SX
;; OPERATING SYSTEM: MS-DOS (Version 5.0)
;; SOFTWARE: WordPerfect (Version 5.1)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/029,022
;; FILING DATE: 19930310
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 809,291
;; FILING DATE: 17 DEC 91
;; APPLICATION NUMBER: 972,135
;; FILING DATE: 05 NOV 92
;; APPLICATION NUMBER: PCT/US92/11008
;; FILING DATE: 17 DEC 92
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rae-Venter, Barbara
;; REGISTRATION NUMBER: 32,750
;; REFERENCE/DOCKET NUMBER: 05935/008001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 854-5277
;; TELEFAX: (415) 854-0875
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 930
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-029-022-2
;
Query Match 46.1%; Score 256; DB 1; Length 930;
Best Local Similarity 97.8%; Pred. NO. 7.9e-48;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY 2 AGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 61
DB 157 AGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 216
OY 62 GTTACATACTTACGGTAATTTGCGCGCGGTGACCGGCCAACGACCCCGCCCATG 121
DB 217 GTTACATACTTACGGTAATTTGCGCGCGGTGACCGGCCAACGACCCCGCCCATG 276
OY 122 AGCTCAATATAGCATGATGTTCCCATATAGCCCAATAGGAGCTTTCATTGAGCTCA 181
DB 277 AGCTCAATATAGCATGATGTTCCCATATAGCCCAATAGGAGCTTTCATTGAGCTCA 336
OY 182 TGGGTGAGATTTTACGTAACCTGCCCA-TTGGCAGTACATCAAGTATCATATGCA 240
DB 337 TGGGTGAGATTTTACGTAACCTGCCCACTGGCAGTACATCAAGTATCATATGCA 396
OY 241 AGTACGCCCTATTGACGTCATATGAGGTAATG 276
DB 397 AGTACGCCCTATTGACGTCATATGAGGTAATG 432

RESULT 7
US-08-029-022-4
; Sequence 4, Application US/08029022
; Patent No. 5641662

GENERAL INFORMATION:
APPLICANT: Debs, Robert J.
TITLE OF INVENTION: TRANSECTION OF LUNG VIA AEROSOLIZED
TITLE OF INVENTION: TRANSENE DELIVERY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/029,022
FILING DATE: 19930310
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 809,291
FILING DATE: 17 DEC 91
APPLICATION NUMBER: 972,135
FILING DATE: 05 NOV 92
APPLICATION NUMBER: PCT/US92/11008
FILING DATE: 17 DEC 92
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Ventler, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 05935/008001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-0875
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 930
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-029-022-4

Query Match 46.1%; Score 256; DB 1; Length 930;
Best Local Similarity 97.8%; Pred. No. 7.9e-48;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 2 AGTTATTAATAGTATCAATTAAGGGGTCATTAGTTCATAGCCCAATATGAGTTCCGC 61
DB 157 AGTTATTAATAGTATCAATTAAGGGGTCATTAGTTCATAGCCCAATATGAGTTCCGC 216
QY 62 GTTACATACTTACGTAATTTGGCCCGCGCTGACGCCCAAGAGCCCCGCCCATTTG 121
DB 217 GTTACATACTTACGTAATTTGGCCCGCGCTGACGCCCAAGAGCCCCGCCCATTTG 276
QY 122 ACGTCAATATAGCATATGTTCCCATAGTAAGCCCAATAGGACCTTCCATGAGTCAA 181
DB 277 ACGTCAATATAGCATATGTTCCCATAGTAAGCCCAATAGGACCTTCCATGAGTCAA 336
QY 182 TGGGTGAGTATTTACGTAAGTCCCA-TTGGCAGTACATCAAGTATCATATAGCCA 240
DB 337 TGGGTGAGTATTTACGTAAGTCCCACTTGGCAGTACATCAAGTATCATATAGCCA 396
QY 241 AGTACGCCCTTATGAGTCAATGACGTAATGG 276
DB 397 AGTACGCCCTTATGAGTCAATGACGTAATGG 432

RESULT 8
US-08-246-376-2
Sequence 2, Application US/08246376

Patent No. 5827703
GENERAL INFORMATION:
APPLICANT: Robert J. Debs
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IN VIVO
TITLE OF INVENTION: GENE THERAPY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,376
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/992,687
FILING DATE: December 17, 1992
APPLICATION NUMBER: 07/927,200
FILING DATE: August 6, 1992
APPLICATION NUMBER: 07/894,498
FILING DATE: June 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Rae-Ventler
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 05935/005051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-0875
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 930
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-246-376-2

Query Match 46.1%; Score 256; DB 1; Length 930;
Best Local Similarity 97.8%; Pred. No. 7.9e-48;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 2 AGTTATTAATAGTATCAATTAAGGGGTCATTAGTTCATAGCCCAATATGAGTTCCGC 61
DB 157 AGTTATTAATAGTATCAATTAAGGGGTCATTAGTTCATAGCCCAATATGAGTTCCGC 216
QY 62 GTTACATACTTACGTAATTTGGCCCGCGCTGACGCCCAAGAGCCCCGCCCATTTG 121
DB 217 GTTACATACTTACGTAATTTGGCCCGCGCTGACGCCCAAGAGCCCCGCCCATTTG 276
QY 122 ACGTCAATATAGCATATGTTCCCATAGTAAGCCCAATAGGACCTTCCATGAGTCAA 181
DB 277 ACGTCAATATAGCATATGTTCCCATAGTAAGCCCAATAGGACCTTCCATGAGTCAA 336
QY 182 TGGGTGAGTATTTACGTAAGTCCCA-TTGGCAGTACATCAAGTATCATATAGCCA 240
DB 337 TGGGTGAGTATTTACGTAAGTCCCACTTGGCAGTACATCAAGTATCATATAGCCA 396
QY 241 AGTACGCCCTTATGAGTCAATGACGTAATGG 276
DB 397 AGTACGCCCTTATGAGTCAATGACGTAATGG 432

RESULT 9
US-08-246-376-4

Sequence 4, Application US/08246376
Patent No. 5827703
GENERAL INFORMATION:
APPLICANT: Robert J. Debs
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IN VIVO
TITLE OF INVENTION: GENE THERAPY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,376
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/992,687
FILING DATE: December 17, 1992
APPLICATION NUMBER: 07/927,200
FILING DATE: August 6, 1992
APPLICATION NUMBER: 07/894,498
FILING DATE: June 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Rae-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 05935/005051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-0875
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 930
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-246-376-4

Query Match 46.1% Score 256; DB 1; Length 930;

Best Local Similarity 97.8%; Pred. No. 7.9e-48; Indels 1; Gaps 1;
Matches 270; Conservative 0; Mismatches 5;

QY 2 AGTATTAATAGTAAATAGCGGGCATATGATCCCATATATGAGTTCCGC 61
DB 157 AGTATTAATAGTAAATAGCGGGCATATGATCCCATATATGAGTTCCGC 216
QY 62 GTTACATACTAGGTAATGCGCGCGCTGACCGCCCAAGACCCCGCCATTG 121
DB 217 GTTACATACTAGGTAATGCGCGCGCTGACCGCCCAAGACCCCGCCATTG 276
QY 122 AGTCATAATAGAGGTATGTTCCCATAGTAAGCCCAATAGGAGCTTTCATTGACGTCAA 181
DB 277 AGTCATAATAGAGGTATGTTCCCATAGTAAGCCCAATAGGAGCTTTCATTGACGTCAA 336
QY 182 TGGGTGAGATTATAGGTAAGTACGCCA-TTGGCAGTACATCAAGGTATCATATGCA 240
DB 337 TGGGTGAGATTATAGGTAAGTACGCCA-TTGGCAGTACATCAAGGTATCATATGCA 396
QY 241 AGTACGCCCTATGAGGTCAATGACGTAATG 276
DB 397 AGTACGCCCTATGAGGTCAATGACGTAATG 432

RESULT 10

US-07-972-135-2
Sequence 2, Application US/07972135
Patent No. 5858784
GENERAL INFORMATION:
APPLICANT: Robert J. Debs
TITLE OF INVENTION: EXPRESSION OF CLONED
TITLE OF INVENTION: GENES IN THE
TITLE OF INVENTION: LUNG BY AEROSOL - AND
TITLE OF INVENTION: LIPOSOE-BASED
TITLE OF INVENTION: DELIVERY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road,
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version
5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,135
FILING DATE: No. 5858784ember 5, 1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/809,291
FILING DATE: December 17, 1991
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Rae-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 05935/007051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-0875
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 930
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-972-135-2

Query Match 46.1% Score 256; DB 2; Length 930;

Best Local Similarity 97.8%; Pred. No. 7.9e-48; Indels 1; Gaps 1;
Matches 270; Conservative 0; Mismatches 5;

QY 2 AGTATTAATAGTAAATAGCGGGCATATGATCCCATATATGAGTTCCGC 61
DB 157 AGTATTAATAGTAAATAGCGGGCATATGATCCCATATATGAGTTCCGC 216
QY 62 GTTACATACTAGGTAATGCGCGCGCTGACCGCCCAAGACCCCGCCATTG 121
DB 217 GTTACATACTAGGTAATGCGCGCGCTGACCGCCCAAGACCCCGCCATTG 276
QY 122 AGTCATAATAGAGGTATGTTCCCATAGTAAGCCCAATAGGAGCTTTCATTGACGTCAA 181
DB 277 AGTCATAATAGAGGTATGTTCCCATAGTAAGCCCAATAGGAGCTTTCATTGACGTCAA 336
QY 182 TGGGTGAGATTATAGGTAAGTACGCCA-TTGGCAGTACATCAAGGTATCATATGCA 240
DB 337 TGGGTGAGATTATAGGTAAGTACGCCA-TTGGCAGTACATCAAGGTATCATATGCA 396
QY 241 AGTACGCCCTATGAGGTCAATGACGTAATG 276
DB 397 AGTACGCCCTATGAGGTCAATGACGTAATG 432

DB 397 AGTACGCCCTATTGACGTCATGACGTAATGCG 432

RESULT 11
US-07-972-135-4

Sequence 4, Application US/07972135
Patent No. 5858784

GENERAL INFORMATION:

APPLICANT: Robert J. Debs

TITLE OF INVENTION: EXPRESSION OF CLONED

TITLE OF INVENTION: GENES IN THE

TITLE OF INVENTION: LONG BY AEROSOL - AND

TITLE OF INVENTION: LIPOSOOME-BASED

TITLE OF INVENTION: DELIVERY

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 2200 Sand Hill Road,

CITY: Menlo Park

STATE: California

COUNTRY: U.S.A.

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM PS/2 Model 502 or

COMPUTER: 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordperfect (Version

SOFTWARE: 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/972,135

FILING DATE: No. 5858784ember 5, 1992

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/809,291

FILING DATE: December 17, 1991

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Barbara Rae-Venter

REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: 05935/007051

TELEPHONE: (415) 854-0875

TELEFAX: (415) 854-5277

TELEPHONE: (415) 854-5277

TELEFAX: (415) 854-5277

TELEPHONE: (415) 854-5277

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TELEPHONE: (415) 854-5277

TELEFAX: (415) 854-5277

TELEPHONE: (415) 854-5277

DB 277 ACCTCAATATATACGATATTTCCCATAGTACGCCCATAGGACTTCCATTACGTCMA 336
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QY 182 TGGGTGAGATATTAGCGTAACCTGCCA-TTGGCAGTACATCAAGTATATATGCGCA 240
|||
DB 337 TGGGTGAGATATTAGCGTAACCTGCCA-TTGGCAGTACATCAAGTATATATGCGCA 396
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QY 241 AGTACGCCCCCTATTGACGTCATGACGGTAATG 276
|||
DB 397 AGTACGCCCCCTATTGACGTCATGACGGTAATG 432
|||

RESULT 13

US-09-006-841-2
; Sequence 2, Application US/09006841
; Patent No. 6468798
; GENERAL INFORMATION:
; APPLICANT: Robert J. Debs
; TITLE OF INVENTION: EXPRESSION OF CLONED
; TITLE OF INVENTION: GENES IN THE
; TITLE OF INVENTION: LONG BY AEROSOL - AND
; TITLE OF INVENTION: LIPOSOME-BASED
; TITLE OF INVENTION: DELIVERY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road,
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,841
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,135
; FILING DATE: No. 6468798ember 5, 1992
; APPLICATION NUMBER: 07/809,291
; FILING DATE: December 17, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara Rae-Venter
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: 05935/007US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-5277
; TELEFAX: (415) 854-0875
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 930
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-006-841-2

Query Match 46.1%; Score 256; DB 4; Length 930;
Best Local Similarity 97.8%; Pred. No. 7.9e-48;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 AGTTATTAATAGTAATCAATTACGGGGTCAATTGTTCTATAGCCCATATATGAGTTCCG 61
|||
DB 157 AGTTATTAATAGTAATCAATTACGGGGTCAATTGTTCTATAGCCCATATATGAGTTCCG 216
|||
QY 62 GTTACATTAATCGGTAATATGCGCGGCTGACCGCCCAAGACGACCCCGCCATTG 121
|||
DB 217 GTTACATTAATCGGTAATATGCGCGGCTGACCGCCCAAGACGACCCCGCCATTG 276
|||

QY 122 ACCTCAATATATACGATATTTCCCATAGTACGCCCATAGGACTTCCATTACGTCMA 181
|||
DB 277 ACCTCAATATATACGATATTTCCCATAGTACGCCCATAGGACTTCCATTACGTCMA 336
|||
QY 182 TGGGTGAGATATTAGCGTAACCTGCCA-TTGGCAGTACATCAAGTATATATGCGCA 240
|||
DB 337 TGGGTGAGATATTAGCGTAACCTGCCA-TTGGCAGTACATCAAGTATATATGCGCA 396
|||
QY 241 AGTACGCCCCCTATTGACGTCATGACGGTAATG 276
|||
DB 397 AGTACGCCCCCTATTGACGTCATGACGGTAATG 432
|||

RESULT 14

US-09-006-841-4
; Sequence 4, Application US/09006841
; Patent No. 6468798
; GENERAL INFORMATION:
; APPLICANT: Robert J. Debs
; TITLE OF INVENTION: EXPRESSION OF CLONED
; TITLE OF INVENTION: GENES IN THE
; TITLE OF INVENTION: LONG BY AEROSOL - AND
; TITLE OF INVENTION: LIPOSOME-BASED
; TITLE OF INVENTION: DELIVERY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road,
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,841
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,135
; FILING DATE: No. 6468798ember 5, 1992
; APPLICATION NUMBER: 07/809,291
; FILING DATE: December 17, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara Rae-Venter
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: 05935/007US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-5277
; TELEFAX: (415) 854-0875
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 930
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-006-841-4

Query Match 46.1%; Score 256; DB 4; Length 930;
Best Local Similarity 97.8%; Pred. No. 7.9e-48;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 AGTTATTAATAGTAATCAATTACGGGGTCAATTGTTCTATAGCCCATATATGAGTTCCG 61
|||
DB 157 AGTTATTAATAGTAATCAATTACGGGGTCAATTGTTCTATAGCCCATATATGAGTTCCG 216
|||
QY 62 GTTACATTAATCGGTAATATGCGCGGCTGACCGCCCAAGACGACCCCGCCATTG 121
|||

Db	217	GTTCATTAACCTTAGCGTAAATAGCGCCGGCGCTGGTGACCGCCACGACCCCGCCATTGG	276
OY	122	ACGTCATTAATGACGATATGTTCCCATAGTAAAGCCCAATPAGGACTTTCATTGACGTCAA	181
Db	277	ACGTCAATTAATGACGATATGTTCCCATAGTAAAGCCCAATPAGGACTTTCATTGACGTCAA	336
OY	182	TGGGTGAGATATTTAGCGTAAACTGCCA-TTGGCAGTACATCAAGTATCATATGCCA	240
Db	337	TGGGTGAGATATTTAGCGTAAACTGCCACTTGGCAATACATCAAGTATCATATGCCA	396
OY	241	AGTACGCCCCCTATTGACGTCAATGACGTAATATGG	276
Db	397	AGTACGCCCCCTATTGACGTCAATGACGTAATATGG	432

RESULT 15
PCT-US93-05366-2
; Sequence 2, Application PC/TUS9305366
; GENERAL INFORMATION.

APPLICANT: Ning Zhu
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IN VIVO
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 2200 Sand Hill Road, Suite 100
 CITY: Menlo Park
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 502 or 55XT
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: Wordperfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/05366
 FILING DATE: 04-JUN-1993
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/992,687
 FILING DATE: December 17, 1992
 APPLICATION NUMBER: 07/927,200
 FILING DATE: August 6, 1992
 APPLICATION NUMBER: 07/894,498
 FILING DATE: June 4, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Barbara Rae-Venter
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: 05935/005051
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 854-5277
 TELEFAX: (415) 854-0875
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 930
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

Query Match	46.1%	Score	256	DB	5	Length	930
Best Local Similarity	97.8%	Pred. Ko.	7.9e-48				
Matches	270	Conservative	0	Mismatches	5	Indels	1
						Gaps	1

0y 2 AGTATTATTAAGTAAATTAACGGGTCATTACTTCAATAGCCCATATATAGAACTTCCGC 61
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157 AGTATTATTAAGTAAATTAACGGGTCATTACTTCAATAGCCCATATATAGAACTTCCGC 216
Db
0y 62 GTTACATTAACCTTACGGTAAATTTGGCCCCCGGCTGACCCCCCAACGACCCCCCCATTG 121

Db	217	GTTCATTAACCTACGGTAATATGGCCGGCCCTGGGCTGACCGCCCAACGACCCCGCCCATTTG	216
Qy	122	ACGTCATTAATGACGTATGTTCCCATAGTAACGCCCAATAGGAGCTTTCATTGACGTCAA	181
Db	277	ACGTCATTAATGACGTATGTTCCCATAGTAACGCCCAATAGGAGCTTTCATTGACGTCAA	336
Qy	182	TGGGTGAGATTAATTCACGTAACCTGCCCA-TTGGCAGTACATCAAGTATTCATATGCCA	240
Db	337	TGGGTGAGATTAATTCACGTAACCTGCCCACTTGGCAGTACATCAAGTATTCATATGCCA	396
Qy	241	AGTACGCCCCCTATTGACGTCAATGACGTAATATGG	276
Db	397	AGTACGCCCCCTATTGACGTCAATGACGTAATATGG	432

Search completed: December 15, 2002, 07:29:25
Job time : 77 secs

Location/Qualifiers

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1.569
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/strain="C57BL/6J"
/db_xref="nlestr:H3006C07-3"
/db_xref="taxon:10090"
/clone="H3006C07"
/clone_1lb="NIA Mouse 15K cDNA Clone Set"
/dev_stage="Clones arrayed from a variety of cDNA libraries"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site.1: SalI; Site.2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dt)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A. 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000; Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
BASE COUNT      150 a      136 c      130 g      153 t
ORIGIN

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Query Match      45.8%; Score 254.4; DB 12; Length 569;
Best Local Similarity 97.5%; Pred. No. 3.5e-45;
Matches 269; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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OY  2 AGTTATTAAATGATCAATTAAGGGGTCATTAGTTCATAGCCCATATATGAGTTCGCG 61
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DB  222 AGTATTAAATGATCAATTAAGGGGTCATTAGTTCATAGCCCATATATGAGTTCGCG 281
OY  62 GTTACATTAATCGGTAATTTGGCCCGCGGCTGACCGCCCAACGACCCCGCCCATTTG 121
    |||||||
DB  282 GTTACATTAATCGGTAATTTGGCCCGCGGCTGACCGCCCAACGACCCCGCCCATTTG 341
OY  122 ACCTGATTAATGACGTATGTTCCCATAGTAAGCCCAATAGGACTTTCATTCAGCTCAA 181
    |||||||
DB  342 ACCTGATTAATGACGTATGTTCCCATAGTAAGCCCAATAGGACTTTCATTCAGCTCAA 401
OY  182 TGGGTGAGATTAATGACGTAACTGCCA-TTGGCAGTACATCAAGTATCATATATGCCA 240
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DB  402 TGGGTGAGATTAATGACGTAACTGCCA-TTGGCAGTACATCAAGTATCATATATGCCA 461
OY  241 AGTACGCCCCCTATTGACGTCAATGACGTAAATGG 276
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DB  462 AGTACGCCCCCTATTGACGTCAATGACGTAAATGG 497

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RESULT 2
AA409312      578 bp      mRNA      linear      EST 26-AUG-1998
LOCUS        EST03748 Mouse 7.5 dpc embryo ectoplacental cone cDNA library Mus
DEFINITION   mammalian expression vector, score = 2136, RNA sequence.
ACCESSION    AA409312
VERSION      AA409312.1 GI:2068663
KEYWORDS     EST.
SOURCE       house mouse.
ORGANISM     Mus musculus.

```

```

REFERENCE
1 (bases 1 to 578)
AUTHORS      Ko,M.S.H., Threlk,T.A., Horton,J.H., Wang,X, Cul,Y., Wang,X., Pryor

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TITLE
JOURNAL
COMMENT
'E., Paris,J., Wells-Smith,J., Fujiwara,H., Yotsumoto,S. and Nakashima,H.
Systematic analyses of mouse genes expressed in embryo implantation site
Unpublished (1997)
Contact: Ko MSH
Center for Molecular Medicine and Genetics
Wayne State University
5047 Guillen Mall, Detroit, MI 48202
Tel: 3135776708
Fax: 3135776200
Email: mskocmb.biosci.wayne.edu
Cloning vector pCI-neo, mammalian expression vector, score = 2136
Seq primer: M13 Forward.
Location/Qualifiers
1.578
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="ATCC (Inhost):1364275"
/db_xref="taxon:10090"
/clone="C0039E08"
/clone_1lb="Mouse 7.5 dpc embryo ectoplacental cone cDNA library"
/sex="unknown"
/tissue_type="ectoplacental cone"
/dev_stage="embryonic day 7.5 postconception"
/note="Organ: embryo; Vector: pSPORT1 (Life Technologies); Site.1: SalI; Site.2: NotI; Total RNAs were extracted from ectoplacental cone of 7.5-dpc embryos. The double-stranded cDNA was synthesized from total RNAs with an Oligo(dt) primer. The library was constructed by Minoru S. H. Ko."

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BASE COUNT      153 a      138 c      130 g      154 t      3 others
ORIGIN

```

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Query Match      45.8%; Score 254.4; DB 9; Length 578;
Best Local Similarity 97.5%; Pred. No. 3.5e-45;
Matches 269; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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OY  2 AGTTATTAAATGATCAATTAAGGGGTCATTAGTTCATAGCCCATATATGAGTTCGCG 61
    |||||||
DB  234 AGTATTAAATGATCAATTAAGGGGTCATTAGTTCATAGCCCATATATGAGTTCGCG 293
OY  62 GTTACATTAATCGGTAATTTGGCCCGCGGCTGACCGCCCAACGACCCCGCCCATTTG 121
    |||||||
DB  294 GTTACATTAATCGGTAATTTGGCCCGCGGCTGACCGCCCAACGACCCCGCCCATTTG 353
OY  122 ACCTGATTAATGACGTATGTTCCCATAGTAAGCCCAATAGGACTTTCATTCAGCTCAA 181
    |||||||
DB  354 ACCTGATTAATGACGTATGTTCCCATAGTAAGCCCAATAGGACTTTCATTCAGCTCAA 413
OY  182 TGGGTGAGATTAATGACGTAACTGCCA-TTGGCAGTACATCAAGTATCATATATGCCA 240
    |||||||
DB  414 TGGGTGAGATTAATGACGTAACTGCCA-TTGGCAGTACATCAAGTATCATATATGCCA 473
OY  241 AGTACGCCCCCTATTGACGTCAATGACGTAAATGG 276
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DB  474 AGTACGCCCCCTATTGACGTCAATGACGTAAATGG 509

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```

RESULT 3
AV645339/c      675 bp      mRNA      linear      EST 15-JAN-2002
LOCUS        AV645339
DEFINITION   AV645339 GLA Homo sapiens cDNA clone GLAAC04 3', mRNA sequence.
ACCESSION    AV645339
VERSION      AV645339.1 GI:9866353
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens

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```

REFERENCE
1 (bases 1 to 675)
AUTHORS      Mamalila; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

AUTHORS		TITLE		JOURNAL		COMMENT	
Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, W., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z., and Han, Z.		Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver		Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)		21625106	
Contact: Zeguang Han		Chinese National Human Genome Center at Shanghai		351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China		Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzeghegc.sh.cn	
This clone is available at CHGC in Shanghai.		Location/Qualifiers		1. 675			
/organism="Homo sapiens"		/db_xref="taxon:9606"		/clone="GLAAC04"		/clone_lib="GLA"	
/tissue_type="corresponding non cancerous liver tissue"		/dev_stage="Adult"		/lab_host="SOLR"		/note="Vector: pbluescript sk(-); Site_1: EcoRI; Site_2: XhoI"	
BASE COUNT		159 a 166 c 177 g 169 t 4 others		ORIGIN			
Query Match		41.7%; Score 231.6; DB 10; Length 675;		Best Local Similarity		93.0%; Pred. No. 2.9e-40;	
Matches		251; Conservative		0; Mismatches		18; Indels 1; Gaps 1;	
OY	8	TAATAGTATCAATTACGGGGTCAATTAGTTCATAGCCCATATATGAGTTCGGCGTTACA	67				
Db	673	TTATAGGATCAANATACGGGGTCAATTAGTTCATATAGCCCATATATGAGTTCGGCGTTACA	614				
OY	68	TAACCTAGCGTAAATTTGGCCGGCGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCA	127				
Db	613	TACTTACGGGTAATATGAGCCCGCTGCTGACCGCCCAACGACCCCGCCCATTTGACGTCA	554				
OY	128	ATAATGAGGTATGTTCCTCATAGTAAGCCCAATATGAGGACTTTCATTTGACGTCAATGCGTG	187				
Db	553	ATAATGAGGTATGTTCCTCATAGTAAGCCCAATATGAGGACTTTCATTTGACGTCAATGCGTG	494				
OY	188	GAGTATTTACGGTAAATGTCGCCA-TTGGCAGTACATCAAGTGTATCATATGCCAAGTACG	246				
Db	493	GAGTATTTACGGTAAATGTCGCCA-TTGGCAGTACATCAAGTGTATCATATGCCAAGTACG	434				
OY	247	CCCCCTATTTGACGTCATATGACGGTAAATGG	276				
Db	433	CCCCCTATTTGACGTCATATGACGGTAAATGG	404				
RESULT 4		AV645353		642 bp		EST 15-JAN-2002	
LOCUS		AV645353/c		GLA Homo sapiens cDNA clone GLAAD06 3', mRNA sequence.			
DEFINITION		AV645353		AV645353			
ACCESSION		AV645353.1		GI:9866367			
VERSION		EST.					
KEYWORDS		human.					
SOURCE		Homo sapiens					
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
REFERENCE		1 (bases 1 to 642)					
AUTHORS		Xiao, H., Qu, J., Liu, F., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, W., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z., and Han, Z.					
TITLE		Insight into hepatocellular carcinogenesis at transcriptome level					

JOURNAL MEDLINE COMMENT	by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919 (ex.45) Fax: 86-21-50801922 Email: hanzeg@chgc.sh.cn This clone is available at CHGC in Shanghai.
FEATURES	Location/Qualifiers
SOURCE	1. .642 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="GUAAD06" /clone_lib="GUA" /tissue_type="corresponding non cancerous liver tissue" /dev_stage="Adult" /lab_host="SOLR" /note="Vector: pbluescript sk(-); site_1: EcoRI; site_2: XhoI"
BASE COUNT	150 a 160 c 168 g 160 t 4 others
ORIGIN	
Query Match	40.4%; Score 224.4; DB 10; Length 642;
Best Local Similarity	93.7%; Pred. No. 1e-38;
Matches 253; Conservative	0; Mismatches 15; Indels 2; Gaps 2;
QY 8	TAATAGTATCAATTTACGGGGTCAATTAGTTCATAGCCCATATAGAGATTCGGGTTACA 67
Db 635	TTATAGGATCAATATACGGGGTCAANTAGTTCATAGCCCATATAGNAGTTCGGGTTACA 576
QY 68	TAACTTACGGTAAATTTGGCCCCGGCGCTGACGCCCAAGACCCCGCCCAATTGACGTCA 127
Db 575	T-ACCTTACGGTAAAGGGGGCCCTGGCTGGACGCCCAAGACCMCGCCCAATTGACGTCA 517
QY 128	ATAATGACGTATGTCCCATAGTAAAGCCCATATAGGAGATTTCCATTTGACGTCAATGGGTG 187
Db 516	ATAATGACGTATGTTCCTATAGTAAAGCCCATATAGGAGATTTCCATTTGACGTCAATGGGTG 457
QY 188	GAGTATTTACGCTAAACTGCCA-TTGGCAGTACATCAAGTATATATATGCGAAGTACG 246
Db 456	AAGATTTTACGCTAAAGTCCACCTGGCAGTACATCAATCAAGTATATATGCGAAGTACG 397
QY 247	CCCCCTATTGACGTCAATGACGCTAAATGG 276
Db 396	CCCCCTATTGACGTCAATGACGCTAAATGG 367
RESULT 5	
AV681528/c	672 bp mRNA linear EST 16-JAN-2002
LOCUS	AV681528
DEFINITION	AV681528 GK A Homo sapiens cDNA clone GRAAB04 5', mRNA sequence.
ACCESSION	AV681528
VERSION	AV681528.1 GI:10283391
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 672) Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Hu, G., Gu, J., Chen, Z., and Han, Z.
TITLE	Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
JOURNAL	21625106
MEDLINE	Contact: Zeguang Han
COMMENT	

Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922

FEATURES

29

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GKAAAB04"
/clone_lbp="GKA"
/tissue_type="hepatocellular carcinoma"
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/lab_host="SOLR"
/notes="Vector: plusescript sk(-); Site_1: EcoRI; Site_2
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BASE COUNT	154 a	168 c	178 g	167 t	5 others
ORIGIN					

Query Match	38.88;	Score 215.4;	DB 10;	Length 672;
Best Local Similarity	89.88;	Pred. No. 9.1e-37;		
Matches 239; Conservative	0;	Mismatches 26;	Indels 1;	Gaps 1.

QY	12	AGTAAATACAGGGGCAATTAATTCATAGGCCAATATATGGAATTCGGGTACATTAAC	71
QY	12		
Db	672	AGTAAATCATTACGGGGGTCAATTAATTCATAGGCCAATATATGGAATTCGGGTACATTAAC	613
QY	72	TTACGGTAAATTTGGCCCGCCGGCTGACCCGCCACAGACCCCCGCCATTTAGCTCAATAA	131
QY	72		
Db	612	TACGGGTAAATTTGGCCCGCCGGCTGACCCGCCACAGACCCCMNGCCCTTTACGCTCAATAA	555
QY	132	TGACGTATGTCCCATAGTAAAGCCCAATAGGAGACTTTCATGACGTCATATGGGTGAGT	191
QY	132		
Db	552	TGACGTATGTCCCATAGTAAAGCCCAATAGGAGACTTTCATGACGTCATATGGGTGAGT	493
QY	192	ATTTACGGTAAACTGCCCCA-TTGGCAGTACATCAAGTATCATATATGCCAAGTACGCCCC	250
QY	192		
Db	492	ATTTACGGTAAACTGCCCCA-TTGGCAGTACATCAAGTATCATATATGCCAAGTACGCCCC	433
QY	251	CTATTGACGTCATGAGGGTAAATGG	276
QY	251		
Db	432	CTATTGACGTCATGAGGGTAAATGG	407

RESULT

LOCUS	AV681458	645 bp	mRNA	linear	EST 16-JAN-2002
DEFINITION	AV681458	GKA Homo sapiens cDNA clone GRAAB07 5', mRNA sequence.			

ORGAN:

.....

AUTHOR

TITLE

COMMENT

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai

FEATURES

Source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GRAB07"
/clone_1fb="CA"
/tissue_type="hepatocellular carcinoma"
/dev_host="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

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BASE COUNT	151 a	163 c	166 g	157 t	8 others
ORIGIN					

Query Match	38.5%;	Score 213.4;	DB 10;	Length 645;
Best Local Similarity	90.4%;	Pred. No. 2.5e-36;		
Matches 245; Conservative	0;	Mismatches 24;	Indels 2;	Gaps 2;

Oy	8	TAAATGTAATCAATTACGGGGTCTAATTAGTCATATGACCATTATGAGGTCCGGTTACA	67
Db	639	TTATAGCATCATCATTACGGGTGCATAAGTTTCTATAGCCCATATATGMAGTTGGGGTTACA	580
Oy	68	TAACTTAGCGTAATATGGCCCCGCC- GGCTGAACGGCCCAACGACCCC GCCCATTTGACTTC	120
Db	579	TAACTTAGCGGGTAAGGGGCCCGCTGGCTGACCGCCACNACNCNMCCCATTTGACGTC	520
Oy	127	AATATATGACGTATGTTCGCATATGTAAGCCCAATATAGGAGCTTTCATTTAGACTCAATGGGT	186
Db	519	AATATATGACGTATGTTCGCATATGTAAGCCCAATATAGGAGCTTTCATTTAGACTCAATGGGT	460
Oy	187	GGAGTATTTAGCGTAAATGCCCA-TTGGCAGTACATCAAGTGATCATATGCCAAGTAC	243
Db	459	GAAATATTTAGCGTAAATCGCCCACTTGCACGTACATCACTAGTATCATATGCCAAGTAC	400
Oy	246	GGCCCCATTTAGACGTCAATGACGGAATGG	276
Db	399	GGCCCCATTTAGACGTCAATGACGGAATGG	369

RESULT 7

LOCUS	AV681502	783 bp	mRNA	linear	EST 16-JAN-2002
DEFINITION	AV681502 GKA Homo sapiens cDNA clone GKAHH01 5', mRNA sequence.				
FEATURES					
ORIGIN					

SOURCE

REFERENCES

TITLE

COMMENT

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..783
/organism="Homo sapiens"
source

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/db_xref="taxon:9606"
/clone="GKAAH01"
/clone_lib="GKA"
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/lab_host="SOLR"
/Note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      198 a      191 c      191 g      201 t      2 others
ORIGIN
Query Match      37.8%; Score 210; DB 10; Length 783;
Best Local Similarity 89.5%; Pred. No. 1.3e-35;
Matches 247; Conservative 0; Mismatches 27; Indels 2; Gaps 2;

OY 2 AGTATTAAATGATCAATTAAGGGGTCTTGTTCATAGCCCATATATGAGTCCGC 61
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DB 720 AGTATTAAATGATCAATTAAGGGGTCTTGTTCATAGCCCATATATGAGTCCGC 662
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 62 GTTACATTAAGTAAATTTGGCCCGCGCTGACCGCCCAAGACCCCGCCATTTG 121
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 661 GTTACATTAAGTAAATTTGGCCCGCGCTGACCGCCCAAGACCCCGCCATTTG 602
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 122 ACCTCAATTAATGACGATGTTCCCATATGATACGCCCAATAGGACTTCCATGACGTCAA 181
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 601 ACCTCAATTAATGACGATGTTCCCATATGATACGCCCAATAGGACTTCCATGACGTCAA 542
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 182 TGGGTGAGATTTTAAAGGTTAACTGCCCA-TTGGCAGTACATCAAGTGTATTCATGCCCA 240
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 541 TGGGTGAGATTTTAAAGGTTAACTGCCCA-TTGGCAGTACATCAAGTGTATTCATGCCCA 482
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 241 AGTACGCCCCCTATTGACGTCATGACGGAATATGG 276
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 481 AGTACGCCCCCTATTGACGTCATGACGGAATATGG 446
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
AV681477/c      676 bp      mRNA      linear      EST 16-JAN-2002
LOCUS      AV681477 GKA Homo sapiens cDNA clone GKAAAB12 5', mRNA sequence.
DEFINITION      AV681477
ACCESSION      AV681477
VERSION      AV681477.1 GI:10283340
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 676)
AUTHORS      Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Ou,J., Liu,F., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Shen,K., Lu,G., Pu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE      Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE      21625106
COMMENT      Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
1. 676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GKAAAB12"
/clone_lib="GKA"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"

```

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/lab_host="SOLR"
/Note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      153 a      174 c      176 g      169 t      4 others
ORIGIN
Query Match      37.4%; Score 207.8; DB 10; Length 676;
Best Local Similarity 91.6%; Pred. No. 4e-35;
Matches 240; Conservative 0; Mismatches 20; Indels 2; Gaps 2;

OY 16 ATCAATTACGGGGTCATTAGTTCATAGCCCATATATGAGTCCCGTTACATTAATAC 75
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 672 ATCAATTACGGGGTCATTAGTTCATAGCCCATATATGAGTCCCGTTACATTAATAC 613
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 76 GGTAAATTGGCCCGCGCTGACCGCCCAAGACCCCGCCATTTGACGTCATTAATGAC 135
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 612 GGTAAATTGGCCCGCGCTGACCGCCCAAGACCCCGCCATTTGACGTCATTAATGAC 553
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 136 GTATGTTCCCATTAATGACGCCCAATAGGACTTTCATTAATGACGTCATTAATGAC 195
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 552 GTATGTTCCCATTAATGACGCCCAATAGGACTTTCATTAATGACGTCATTAATGAC 494
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 196 ACCTTAATCTGCCCA-TTGGCAGTACATCAAGTGTATTCATTAATGACGTCATTAAT 254
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 493 ACCTTAATCTGCCCA-TTGGCAGTACATCAAGTGTATTCATTAATGACGTCATTAAT 434
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 255 TGACGTCATTAATGACGTCATTAATGAC 276
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 433 TGACGTCATTAATGACGTCATTAATGAC 412
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
AV645377/c      619 bp      mRNA      linear      EST 15-JAN-2002
LOCUS      AV645377 GLA Homo sapiens cDNA clone GLAABF06 3', mRNA sequence.
DEFINITION      AV645377
ACCESSION      AV645377
VERSION      AV645377.1 GI:9866391
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 619)
AUTHORS      Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Ou,J., Liu,F., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Shen,K., Lu,G., Pu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE      Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE      21625106
COMMENT      Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
1. 619
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLAABF06"
/clone_lib="GLA"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/Note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      142 a      158 c      162 g      148 t      9 others
ORIGIN

```

Query Match	Best Local Similarity	Score	205.8	DB 10	Length	619
Query Match	Best Local Similarity	89.4%	Pred. No. 11e-34			
Matches	227	Conservative	0	Matches	26	Indels 1; Gaps 1
0Y	24	CGGGGTCATTATTCATATGATCCCATATATATGATATGATCCGCGTACATATACGTAAATTT	83			
Db	619	CGGGGTCATTATTCATATGATCCCATATATATGATATGATCCGCGTACATATACGTAAATG	560			
0Y	84	GGCCCGCCGGCTGACCCGCCAACAAGCCCCGCCCATTTGACGTCAATATAGCATATGTC	143			
Db	559	GGCCCGCCGGCTGACCCGCCAACAAGCCCCGCCCATTTGACGTCAATATAGCATATGTC	500			
0Y	144	CCATGTATACGGCATATAGGACTTTCATATGACGTCAATGAGGTGAGATTTAAGCTTAA	203			
Db	499	CCATGTATACGGCATATAGGACTTTCATATGACGTCAATGAGGTGAGATTTAAGCTTAA	440			
0Y	204	CTGCCCA-TTGGCAGTACATCAATGATATCATATATGCAAGTACGCCCTTATGAGCTCA	262			
Db	439	CTGCCCACTTGGCATATCATATGATATCATATATGCAAGTACGCCCTTATGAGCTCA	380			
0Y	263	ATGACGCTAATGG 276				
Db	379	ATGACGCTAATGG 366				
RESULT 10	BQ247946/c					
LOCUS	BQ247946	525 bp	mRNA	linear	EST 03-MAY-2002	
DEFINITION	TAE25015A06F TAE25 Triticum aestivum cDNA clone TAE25015A06F, mRNA					
ACCESSION	BQ247946					
VERSION	BQ247946.1	GI:20443822				
KEYWORDS	EST.					
SOURCE	bread wheat.					
ORGANISM	Triticum aestivum					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poidea					
JOURNAL	1 (bases 1 to 525)					
COMMENT	Cloutier,S. Wheat functional genomics - glenlea developing seeds cDNA libraries Unpublished (2002) Contact: Dr. Sylvie Cloutier Cereals Research Centre, Agriculture and Agri-Food Canada 195 Dufresne Rd. Winnipeg, MB, Canada R3T 2M5 Tel: (204) 983-2340 Fax: (204) 983-4604 Email: scloutier@em.agr.ca was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >870 bp Plate: 015 Row: A Column: 06 Seq primer: M13 Forward. Location/Qualifiers 1..525 /organism="Triticum aestivum" /cultivar="Glenlea" /db_xref="taxon:4565" /clone="TAE25015A06F" /clone_11b="TAE25" /tissue="type="developing seeds" /dev_stage="25 days after anthesis" /lab_host="E. coli DH108" /note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies); Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 25 days post-anthesis"					
BASE COUNT	140 a	113 c	133 g	139 t		
ORIGIN						
Query Match	Best Local Similarity	35.9%	Score 159.2	DB 14	Length 525	
Matches	233	Conservative	0	Matches	36	Indels 1; Gaps 1

OY	6	ATTATAGTAATCAATTTACGGGGTCATATTAGTTCATAGCCCATATATGAGAGTTCCGGCTTA	65
Db	503	ATTAAACCTATAAAATGAGCGTATTACAGAGGCCCTTTACACGCATTAAGATGATGCTTA	444
OY	66	CATACATTCAGGTAATTTGGCCCGCGGTGACGCCCAAGACGCCCGCCCATATGAGT	125
Db	443	CATACCTTACGGTAATATGGCCCGCGTGGCTGACGCCCAAGACGCCCGCCCATATGAGT	384
OY	126	CAATTAATGACGTATGTTCCCATAGTAAGCCCAATAGGACATTTCCATTTAGAGTCATG	185
Db	383	CAATTAATGACGTATGTTCCCATAGTAAGCCCAATAGGACATTTCCATTTAGAGTCATG	324
OY	186	TGGATATTTTACGGTAACCTGCCA-TTGGCAGTATCATCAGTGTATATATGCCAATA	244
Db	333	TGGATATTTTACGGTAACCTGCCA-TTGGCAGTATCATCAGTGTATATATATGCCAATA	264
OY	245	CGCCCCCTATTGAGCTCAATGACGTAATATG	276
Db	263	CGCCCCCTATTGAGCTCAATGACGTAATATG	232

RESULT 11

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

BC899290

401 bp

mRNA

linear

EST 06-NOV-2001

BC899290

HOA18-1-14 HOA (Human Osteoarthritis Cartilage)

Homo sapiens cDNA, mRNA sequence.

BC899290

BC899290.1

GI:14309539

EST.

human.

Homo sapiens

Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 401)

Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathya,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritis cartilage cDNA libraries

Osteoarthr. Cartil. 9 (7), 641-653 (2001)

Contact: Sanjay Kumar

UM2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-1@sk.com

Location/Qualifiers

1. 401

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HOA (Human Osteoarthritis Cartilage)"

/tissue_type="cartilage"

/lab_host="E.coli DH10 B"

/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI; Directional"

BASE COUNT

100 a 114 c 97 g 90 t

ORIGIN

Query Match 35.28; Score 195.4; DB:12; Length 401; Best Local Similarity 96.88; Pred. No.1.9e-32; Matches 210; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

61

CGTTTCATACCTTACGTAATTTGGCCCGCGGTGACGCCCAAGACGCCCGCCCATTT

120

123

CGTGCATTAACCTTACGTAATTTGGCCCGCGGTGACGCCCAAGACGCCCGCCCATTT

182

121

GACGTCAATTAATGACGTATGTTCCCATAGTAAGCCCAATAGGACTTTCATTCAGCTCA

180

Db 183 GACGTAATTAATGACGATTTCCCAATGTAAGCCCAATGAGGACCTTCCATGACGTCA 242

QY 181 ATGGGTGAGTATTTACGGTAACATGCCCCA-TTGGACAGTACATCAATGATATATATGCC 239
|||||
Db 243 ATGGGTGAGTATTTACGGTAACATGCCCCA-TTGGACAGTACATCAATGATATATATGCC 302

QY 240 AAGTACGCCCCCTATGACGTCAATGACGTAATG 276
|||||
Db 303 AAGTACGCCCCCTATGACGTCAATGACGTAATG 339

RESULT 12
AV681519/c 821 bp mRNA linear EST 16-JAN-2002
LOCUS AV681519 GRK Homo sapiens cDNA clone GKAAAG03 5', mRNA sequence.
DEFINITION AV681519
ACCESSION AV681519
VERSION AV681519.1 GI:10283382
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 821)
AUTHORS Xu,X., Huang,D., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1. 821
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GKAAAG03"
/clone_1lb="GKA"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
KhoI"
BASE COUNT 216 a 198 c 206 g 193 t 8 others
ORIGIN

Query Match 35.2%; Score 195.2; DB 10; Length 821;
Best Local Similarity 83.0%; Pred. No. 2, 1e-32;
Matches 229; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

QY 2 AGTATTATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 61
|||||
Db 729 AGTATTATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 670

QY 62 GTTACATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 121
|||||
Db 669 TTACATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 610

QY 122 ACCTCAATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 181
|||||
Db 609 ACCTCAATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 550

QY 182 TGGGTGAGTATTTACGGTAACATGCCCCA-TTGGACAGTACATCAATGATATATATGCC 240
|||||
Db 549 TGGGTGAGTATTTACGGTAACATGCCCCA-TTGGACAGTACATCAATGATATATATGCC 490

QY 241 AGTACGCCCCCTATGACGTCAATGACGTAATG 276
|||||
Db 489 AGTACGCCCCCTATGACGTCAATGACGTAATG 454

RESULT 13
AV681464/c 806 bp mRNA linear EST 16-JAN-2002
LOCUS AV681464 GRK Homo sapiens cDNA clone GKAAAG10 5', mRNA sequence.
DEFINITION AV681464
ACCESSION AV681464
VERSION AV681464.1 GI:10283327
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 806)
AUTHORS Xu,X., Huang,D., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1. 806
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GKAAAG10"
/clone_1lb="GKA"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
KhoI"
BASE COUNT 199 a 200 c 208 g 191 t 8 others
ORIGIN

Query Match 35.0%; Score 194; DB 10; Length 806;
Best Local Similarity 83.0%; Pred. No. 3, 8e-32;
Matches 229; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

QY 2 AGTATTATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 61
|||||
Db 744 AGTATTATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 685

QY 62 GTTACATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 121
|||||
Db 684 GTTACATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 625

QY 122 ACCTCAATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 181
|||||
Db 624 ACCTCAATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCGC 565

QY 182 TGGGTGAGTATTTACGGTAACATGCCCCA-TTGGACAGTACATCAATGATATATATGCC 240
|||||
Db 564 TGGGTGAGTATTTACGGTAACATGCCCCA-TTGGACAGTACATCAATGATATATATGCC 505

QY 241 AGTACGCCCCCTATGACGTCAATGACGTAATG 276
|||||
Db 504 AGTACGCCCCCTATGACGTCAATGACGTAATG 469

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 05:41:10 ; Search time 3127 Seconds

(without alignments)
5165.352 Million cell updates/sec

Title: US-10-059-152-1

Sequence: 1 gatttataataatgaatca.....cgcctcgtactgaccgcgc 555

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
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28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_in:*
32: em_htg_lav:*
33: em_htg_other:*
34: em_htg_mus:*
35: em_htg_pin:*
36: em_htg_rod:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	530	95.5	561	6	E51988	E51988 Promoter, r
2	315.6	56.9	5894	12	AF334827	AF334827 Cloning v
3	309.4	55.7	4211	6	BD012722	BD012722 Mammalian
4	309.4	55.7	4211	23	BD005270	BD005270 Mammalian
5	309.4	55.7	5100	6	AX468471	AX468471 Sequence
6	309.4	55.7	6148	6	AX468470	AX468470 Sequence
7	257	46.3	599	6	E51990	E51990 Promoter, r
8	256	46.1	590	6	E59416	E59416 Signal Pept
9	256	46.1	777	6	BD000145	BD000145 Vector ha
10	256	46.1	777	6	I05430	I05430 Sequence 16
11	256	46.1	777	6	I08105	I08105 Sequence 3
12	256	46.1	919	6	BD000143	BD000143 Vector ha
13	256	46.1	919	6	I05393	I05393 Sequence 14
14	256	46.1	919	6	I08103	I08103 Sequence 1
15	256	46.1	930	6	AR028792	AR028792 Sequence
16	256	46.1	930	6	AR028794	AR028794 Sequence
17	256	46.1	930	6	AR050544	AR050544 Sequence
18	256	46.1	930	6	AR050546	AR050546 Sequence
19	256	46.1	930	6	AR094363	AR094363 Sequence
20	256	46.1	930	6	I49834	I49834 Sequence 2
21	256	46.1	930	6	I49836	I49836 Sequence 4
22	256	46.1	930	14	HS51EE	K03104 Human clyom
23	256	46.1	1078	6	A92081	A92081 Sequence 5
24	256	46.1	1318	6	A92080	A92080 Sequence 4
25	256	46.1	1417	6	A92077	A92077 Sequence 1
26	256	46.1	1645	6	A92078	A92078 Sequence 2
27	256	46.1	1767	6	AX402407	AX402407 Sequence
28	256	46.1	1848	14	HEHCMP1	X03922 Human clyom
29	256	46.1	1870	6	A92079	A92079 Sequence 3
30	256	46.1	2129	6	A01324	A01324 Human clyom
31	256	46.1	2133	6	A01323	A01323 Human clyom
32	256	46.1	2355	12	AF192534	AF192534 Expressio
33	256	46.1	3506	12	AF416744	AF416744 Cloning v
34	256	46.1	3602	12	AF327894	AF327894 Cloning v
35	256	46.1	3610	6	AX030966	AX030966 Sequence
36	256	46.1	3643	12	AF327895	AF327895 Expressio
37	256	46.1	3903	6	AX076478	AX076478 Sequence
38	256	46.1	3987	6	AR182910	AR182910 Sequence
39	256	46.1	3987	6	AR182911	AR182911 Sequence
40	256	46.1	4050	12	AF053407	AF053407 Expressio
41	256	46.1	4072	6	AX205074	AX205074 Sequence
42	256	46.1	4187	12	AF151087	AF151087 Cloning v
43	256	46.1	4201	6	AX076477	AX076477 Sequence
44	256	46.1	4207	6	AX359930	AX359930 Sequence
45	256	46.1	4207	6	AX382144	AX382144 Sequence

ALIGNMENTS

RESULT 1
E51988
LOCUS E51988 561 bp DNA linear PAT 31-JAN-2002
DEFINITION Promoter, recombinant containing the same and utilization thereof.
ACCESSION E51988
VERSION E51988.1 GI:18629549
KEYWORDS JP 2001000188-A/3.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 561)
AUTHORS Kubomura, M. and Saito, S.
TITLE Promoter, recombinant containing the same and utilization thereof
JOURNAL Patent: JP 2001000188-A 3 09-JAN-2001;
NIPPON ZEON CORP

COMMENT OS Artificial Sequence
 PN JP 2001000188-A/3
 PD 09-JAN-2001
 PF 22-JUN-1999 JP 1999174804
 PR MAYUMI KUBOMURA, SHUJI SAITO
 PI C12N15/09, A61K31/00, A61K31/00, A61K39/02, A61K39/17, A61K39/215,
 PC C07K14/125,
 PC C07K14/165, C07K14/30, C12N7/00, C12N15/00
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 FH
 FT source location/Qualifiers
 1.561
 /organism="Artificial Sequence",
 location/Qualifiers
 1.561
 /db_xref="taxon:32630",
 /organism="synthetic construct"

BASE COUNT 109 a 156 c 191 g 105 t

ORIGIN

Query Match 95.5%; Score 530; DB 6; Length 561;
 Best Local Similarity 99.5%; Pred. No. 4.9e-95;
 Matches 553; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

QY 2 AGTTATTAATAGTAATCAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 61
 DB 1 AGTTATTAATAGTAATCAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 60
 QY 62 GTTACATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 121
 DB 61 GTTACATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 119
 QY 122 AGTCAATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 181
 DB 120 AGTCAATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 179
 QY 182 TGGGTGAGATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 241
 DB 180 TGGGTGAGATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 239
 QY 242 GTTACATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 301
 DB 240 GTTACATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 299
 QY 302 GGC--GG 359
 DB 300 GGC--GG 359
 QY 360 CGAGGGGAGAGGTGG 419
 DB 360 CGAGGGGAGAGGTGG 419
 QY 420 TGGCGAGGG 479
 DB 420 TGGCGAGGG 479
 QY 480 CTCGCGGCTGCTTCG 539
 DB 480 CTCGCGGCTGCTTCG 539
 QY 540 TCTGACTGACCGGTC 555
 DB 540 TCTGACTGACCGGTC 555

RESULT 2
 AF334827 5894 bp DNA circular STM 20-FEB-2001
 LOCUS Cloning vector pTurbo-Cre, complete sequence.
 DEFINITION AF334827
 ACCESSION AF334827.1 GI:12965137
 VERSION
 KEYWORDS Cloning vector pTurbo-Cre.
 SOURCE

ORGANISM Cloning vector pTurbo-Cre
 artificial sequences: vectors.
 REFERENCE 1 (bases 1 to 5894)
 AUTHORS Lu, Z.H., Graber, T.A. and Ley, T.J.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-2001) Division of Oncology, Section of Stem Cell Biology, Washington University School of Medicine, 660 South Euclid Avenue, Campus Box 8007, St. Louis, MO 63110-1093, USA
 Location/Qualifiers
 1.5894
 /organism="Cloning vector pTurbo-Cre"
 /db_xref="taxon:152298"
 1.364
 /note="cytomegalovirus immediate early region"
 365..646
 /note="chicken beta-actin"
 647..1619
 /note="chicken beta-actin"
 1620..1664
 /note="rabbit beta-globin"
 1742..2797
 /note="contains nuclear localization signal; Cre recombinase"
 /codon_start=1
 /transl_table=11
 /product="cre recombinase"
 /protein_id="AAK11472.1"
 /db_xref="GI:12965138"
 /transl_table=11
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 1742..1768
 /note="Region: nuclear localization signal; NLS"
 2818..3344
 /note="rabbit beta-globin"
 complement(485..5745)
 /note="amp resistance"
 /codon_start=1
 /transl_table=11
 /product="ampicillin resistance protein"
 /protein_id="AAK11473.1"
 /db_xref="GI:12965139"
 /transl_table=11
 /product="MSIOHFRVLAIPFAAFCIPVFAHETLVKRVDAEDQLGARVY IELDLSGKILSFREPRFPWMTSTFKVLLGAVLRIDAGQOLARRIRHISQNDLYE VSPVREKHLIDEMTVRELCSAITSNDNRANLLRTTGSGKRELTAFIHMGGHTRRL DMWEPLNLAIRPDERDTPPYAMATTLKRLTGLTSLASRQQLIDMEADRYAEP LINSALPAGNFIADKRSAGNRSGLIALLGPDPKPSRIIVYITVTSQATWDERNRQIA EIGASLIRKHM"

BASE COUNT 1279 a 1522 c 1645 g 1448 t

ORIGIN

Query Match 56.9%; Score 315.6; DB 12; Length 5894;
 Best Local Similarity 74.9%; Pred. No. 1.1e-52;
 Matches 544; Conservative 0; Mismatches 9; Indels 173; Gaps 5;

QY 2 AGTTATTAATAGTAATCAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 61
 DB 4 AGTTATTAATAGTAATCAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 63
 QY 62 GTTACATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 121
 DB 64 GTTACATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 123
 QY 122 AGTCAATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 181
 DB 124 AGTCAATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 183
 QY 182 TGGGTGAGATTAATTAAGTAATTCAGGGGTCATTGTTCCATAGCCCATATATAGAGTCCGC 240

	Query Match	55.7%;	Score 309.4;	DB 6;	Length 4211;	
	Best Local Similarity	74.6%;	Pred. No. 1;8e-51;	Mismatches 0;	Indels 173;	Gaps 5;
	Matches 539;	Conservative				
OY	2 AGTATTAAAGTAATCAATTACGGGCGCATTTACTTCATACCCATAATATGAGTCTCCG	61				
Db	138 AGTATTAAAGTAATCAATTACGGGCGCATTTACTTCATACCCATAATATGAGTCTCCG	197				
OY	62 GTTACATACCTAGAGTAATTTGGCCGCCGTGCACGCCCAAGACCOCGCCCATTTG	121				
Db	198 GTTACATACCTAGAGTAATTTGGCCGCCGTGCACGCCCAAGACCOCGCCCATTTG	257				
OY	122 ACGTCAATPATGACGTATGTTCCCATAGTAAGCCCAATAGGAGCTTTCATTGACGTAA	181				
Db	258 ACGTCAATPATGACGTATGTTCCCATAGTAAGCCCAATAGGAGCTTTCATTGACGTAA	317				
OY	182 TTGGTGAGATTTAAGCTAACAGTCCCA--TTGGCAGATACAAGTATCATATGCCA	240				
Db	318 TTGGTGAGATTTAAGCTAACAGTCCCACTGGCAGTACATCAAGTATCATATGCCA	377				
OY	241 AGTAGCCCCCTATTGACGTCAATAGCGGTAAATGG-----	276				
Db	378 AGTAGCCCCCTATTGACGTCAATAGCGGTAAATAGGCCCGCGTGGCATTATGCCAGTAG	437				
OY	277 -----	276				
Db	438 ATGACCTTATGGACTTCTACTTGGCGATCATCATGATTATGATCATGCTATTAC	497				
OY	277 -----	276				
Db	498 ATGGGTGAGGTGAGCCCAAGTCTGCTTCTACCTCCCAATCTCCCCCTCCCACAC	557				
OY	277 -----ATGCAATTTTTTTGTGCAGCGATGGGGC--GGGGGGG	311				
Db	558 CCCAATTTTGTATTATTATTATTTTAAATTTTGTGCAGCGATGGGGGGGGGGGGGG	617				
OY	312 GGGGGCGCGCCCAAGCGGGCGGGCGAGAGGGCGGGCGGGCGGAGCGGAGAG	371				
Db	618 GGGGGCGCGCCCAAGCGGGCGGGCGAGAGGGCGGGCGGGCGGAGCGGAGAG	677				
OY	372 GTGGCGCGCGCACCAATAGAAGCGGGCGGCTCCGAAATTTCTTTATATGGGAGCGGC	431				
Db	678 GTGGCGCGCGCACCAATAGAAGCGGGCGGCTCCGAAATTTCTTTATATGGGAGCGGC	737				
OY	432 GGCGGCGCGGCCCATATAAAAGCAAGCGGGCGGGCGGGAGTCTCGCGCCTGCAC	491				
Db	738 GGCGGCGCGGCCCATATAAAAGCAAGCGGGCGGGCGGGAGTCTCGCGCCTGCAC	795				
OY	492 TTCGCCCCCGTCCCGCTCCGCGCGCGCTCGCGCGCGCGCGCGCGCGCTGACGTACCG	551				
Db	796 TTCGCCCCCGTCCCGCTCCGCGCGCGCGCTCCGCGCGCGCGCGCGCGCTGACGTACCG	854				
OY	552 CGT 554 					
Db	855 CGT 857					
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RESULT 4						
BD005270						
ID	BD005270	standard;	DNA;	SYN:	4211 BP.	
XX	BD005270;					
XX	BD005270.1					
XX	SV					
DT	08-FEB-2002 (Rel. 70, Created)					
DT	08-FEB-2002 (Rel. 70, Last updated, Version 1)					
XX	DE	Mammalian model for diabetes.				
XX	KM	JP 03074399-1/2.				

XX		synthetic construct	
OS		artificial sequence.	
CC			
XX	(1)		
RN	1-4211		
RA	Ishino F., Miyoshi N., Ishino T., Yokoyama M., Wakana S.;		
RP	"Mammalian model for diabetes";		
RT	Patent number JP03074399-T/2, 12-JAN-2001.		
RL	JAPAN SCIENCE AND TECHNOLOGY CORP.		
RU			
XX			
CC	Artificial Sequence		
CC	PJ 03074399-T/2		
CC	PD 12-JAN-2001		
CC	PF 18-AUG-2000 JP 2000005546		
CC	PR 20-OCT-1999 JP 99P 298273		
CC	PI FUMIYOSHII ISHINO,NAOKI MIYOSHII,TOMOKO ISHINO,MINESURE		
CC	YOKOYAMA,		
CC	PI SHIGEHARU WAKANA		
CC	PC A01K67/027,C12N15/12,C12Q1/68,C12Q1/02,A61K45/00,A61P3/10,		
CC	G01N33/50,		
CC	G01N33/15		
CC	Key Location/Qualifiers		
CC	FT source 1..4211 /organism="Artificial Sequence"		
PH	Key Location/Qualifiers		
FT	source 1..4211 /db_xref="taxon:32630"		
FT	/organism="synthetic construct"		
XX	Sequence 4211 BP; 890 A; 1139 C; 1230 G; 952 T; 0 other;		
SQ			
	Query Match 55.7% ; Score 309.4; DB: 23; Length 4211;		
	Best Local Similarity 74.6% Pred. No. 1.8e-51;		
	Matches 539; Conservative 0; Mismatches 11; Indels 173; Gaps		
OY	2 AGTTATTAAGTAAATCATTACGGGTCATTAGTCAATAGGCCCATATATGAGATTCGC	61	
Dd			
	138 AGTATTAATGAATATCAATATCACGGGTCATTAGTCAATAGGCCCATATATGAGATTCGC	197	
OY	62 GTTACATACTTAGCGTAATATGCCCCCGCGGTGACGCGCCACGACCCCCTCCCATTTG	121	
Dd			
	198 GTTACATACTTAGCGTAATATGCCCCCGCGGTGACGCGCCACGACCCCCTCCCATTTG	257	
OY	122 ACGTCATAAATGACTATGTTCCTATATAGCGCAATATGAGACTTTCATTGACGTCAA	181	
Dd			
	258 ACGTCATAAATGACTATGTTCCTATATAGCGCAATATGAGACTTTCATTGACGTCAA	317	
OY	182 TGCGTGAGATTAATTCGCTAACCTGCCA--TTGGCAGTACATCAAGTATCATATGGCA	240	
Dd			
	318 TTGGTGAGATTAATTCGCTAACCTGCCA--TTGGCAGTACATCAAGTATCATATGGCA	377	
OY	241 AGTACGCCCTTATTTGACGTCAATACGCGTAATATG-----	276	
Dd			
	378 AGTACGCCCTTATTTGACGTCAATACGCGTAATATG-----	437	
OY	277 -----	276	
Dd	438 ATGACCTTATGAGACTTCTACTTGCGAGTACATCTAGTATAGTCAATGCTATTACC	497	
OY	277 -----	276	
Dd	498 ATGGTCGAGGTGAGCCCCCAGCTTCTGCTTCACTTCCCCATCTCCCCCTCCCAACC	557	
OY	277 -----ATGCAATATTTTGTGCAAGCATGGGGG--GGGGGG	311	
Dd	558 CCCAATTTTGTATTTATTTATTTTTTAAATATTTTGTGACAGCATGGGGGCGGGGGAGG	617	
OY	312 GGGGGCGGGCGCCAAGGGGGGGGGGGGGGGGAGAGGGGGGGGGGAGGCGGAGAG	371	

D	b	618	GCGGGGCGGCCGCACAGCGGGGGCGGGGGGCGAGGGCGGGGGCGGCGAAGCGGGAAGG	677
O	y	372	GTGCGGCGGCAACCATCAGAGCGGCGGCTCCGAAATTTCCTTTATATGCGAGGCGGC	431
D	b	678	GTGCGGCGGCAACCATCAGAGCGGCGGCTCCGAAAGTTTCTTTATATGCGAGGCGGC	737
O	y	432	GCGGCGGCGGCGCCATATAAAGCGAAGCGGCGGCGGCGGAGTGCGCTGCGGCTGCG	491
D	b	738	GCGGCGGCGGCGCCATATAAAGCGAAGCGGCGGCGGCGGAGTGCGCT--GCGTTGCG	795
O	y	492	TTCGCCCCGTGCCCCGCTCCGCGCGCGCTCCGCGCGCCCGCGCGGCTCTACTATGACG	551
D	b	796	TTCGCCCCGTGCCCCGCGCTCCG--CGCGCGCTCCGCGCGCCCGCGCGCTCTACTATGACG	854
O	y	552	CGT 554	
D	b	855	CGT 857	
RESULT 5				
L	OCUS	AX468471	5100 bp	DNA linear PAT 16-JUL-2002
D	EFINITION	Sequence 14 from Patent WO0222834.		
A	CCESSION	AX468471		
V	ERSION	AX468471.1 GI:21901307		
K	EYWORDS	synthetic construct. synthetic construct artificial sequences.		
S	OURCE			
O	RGANISM			
R	EFERENCE	1		
A	UTHORS	Siebel,C. and Brennan,T.J.		
T	ITLE	Methods of producing cells and animals comprising targeted gene modifications		
J	OURNAL	Patent: WO 0222834-A 14 21-MAR-2002; Deltagen, Inc. (US)		
F	EATURES	Location/Qualifiers		
S	ource	1..5100 /organism="synthetic construct" /db_xref="taxon:32630" /note="Construct Sequence"		
B	ASE COUNT	1124 a 1357 c 1475 g 1144 t		
O	RIGIN			
Q	Uery Match	55.7%; Score 309.4; DB 6; Length 5100;		
B	est Local Similarity	74.6%; Pred. No. 1.8e-51;		
M	atches 539; Conservative	0; Mismatches 11; Indels 173; Gaps 5;		
O	y	2 AGTTTATATAGTAATCATATACGGGGGTCATTAGTTTCATAGCCCATATATGAGTTCCG	61	
D	b	59 AGTTTATATAGTAATCATATACGGGGGTCATTAGTTTCATAGCCCATATATGAGTTCCG	118	
O	y	62 GTTACATACCTAGAGGTAATATGGCCGCGGCTGACCGCCCAAGACCCCAGCCATTG	121	
D	b	119 GTTACATACCTAGAGGTAATATGGCCGCGGCTGACCGCCCAAGACCCCAGCCATTG	178	
O	y	122 ACGTCATATAGACGTATGTTCCCATATAGTAAGCCCAATAGGAGCTTTCATTAGAGCTCA	181	
D	b	179 ACGTCATATAGACGTATGTTCCCATATAGTAAGCCCAATAGGAGCTTTCATTAGAGCTCA	238	
O	y	182 TGGGTGAGATATTAACGGTAACGCGCCA-TTGGCAGTACATCAAGTATCATATGCGCA	240	
D	b	239 TGGGTGAGATATTAACGGTAACGCGCCCACTTGGCAGTACATCAAGTATCATATGCGCA	298	
O	y	241 AGTAGCCCCCATATGAGCTCAATAGCGTAATG-----	276	
D	b	299 AGTAGCCCCCATATGAGCTCAATAGCGTAATGCCCCGCTGCAATTAGCCAGTAGC	358	
O	y	277 -----	276	
D	b	359 ATGACCTTAGCGGACTTTCCTACTGTCGAGTACATCTACGTATTAGTATCGCTATTACC	418	
O	y	277 -----	276	

[illegible]

Matches 271; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 GAGTATTATATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCG 60
 DB 6 GAGTATTATATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCG 65

QY 61 CGTTACATTAACGTAAGTAAATGCGCCGCGCTGACGCCACCCAGACCCCGCCATT 120
 DB 66 CATTACATTAACGTAAGTAAATGCGCCGCGCTGACGCCACCCAGACCCCGCCATT 125

QY 121 GAGTCATTAATGACGTAAGTTCCTCCATAGTAACGCCAATAGGACTTTCATTGAGCTCA 180
 DB 126 GAGTCATTAATGACGTAAGTTCCTCCATAGTAACGCCAATAGGACTTTCATTGAGCTCA 185

QY 181 ATGGGTGAGATTAATGAGTAACTGCCCCA-TTGGCAGTACATCAAGTATCATATGCG 239
 DB 186 ATGGGTGAGATTAATGAGTAACTGCCCCA-TTGGCAGTACATCAAGTATCATATGCG 245

QY 240 AAGTACGCCCCCTATGAGTCAATGAGCGTAATG 276
 DB 246 AAGTACGCCCCCTATGAGTCAATGAGCGTAATG 282

RESULT 8
 E59416
 LOCUS E59416 590 bp DNA linear PAT 31-JAN-2002
 DEFINITION Signal peptide.
 ACCESSION E59416
 VERSION E59416.1 GI:18622549
 KEYWORDS JP 2000354490-A/3.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 590)
 AUTHORS Hawkins, R. and Nakamura, M.
 TITLE Signal peptide
 JOURNAL Patent: JP 2000354490-A 3 26-DEC-2000;
 TOTOYA MOTOR CORP
 OS Cauliflower mosaic virus promoter
 PN JP 2000354490-A/3
 PD 26-DEC-2000
 PR 15-JUN-1999 JP 1999168271
 PI RICHARD HAWKINS, MICHIO NAKAMURA
 PC C12N15/09, C07K14/61, C12N1/13, C12P21/02, C12N15/00 CC
 FH key Location/Qualifiers
 FT source 1..590
 FEATURES
 source Location/Qualifiers
 1..590
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 149 a 143 c 141 g 157 t

ORIGIN

Query Match 46.1%; Score 256; DB 6; Length 590;
 Best Local Similarity 97.8%; Pred. No. 7.1e-41;
 Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

DB 182 TGGGTGAGATTAATGAGTAACTGCCACTGACATCATCAAGTATCATATGCCA 241

QY 241 AGTACGCCCCCTATGAGTCAATGAGCGTAATG 276
 DB 242 AGTACGCCCCCTATGAGTCAATGAGCGTAATG 277

RESULT 9
 BD000145
 LOCUS BD000145 777 bp DNA linear PAT 31-JAN-2002
 DEFINITION Vector having stabilized sequence and eucaryotic host cell.
 ACCESSION BD000145
 VERSION BD000145.1 GI:18623224
 KEYWORDS JP 2000308497-A/3.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 777)
 AUTHORS Goman, C.M.
 TITLE Vector having stabilized sequence and eucaryotic host cell
 JOURNAL Patent: JP 2000308497-A 3 07-NOV-2000;
 GENETIC INC
 OS Unidentified
 PN JP 2000308497-A/3
 PD 07-NOV-2000
 PR 17-APR-2000 JP 2000115248
 PR 12-SEP-1986 US 907185, 09-JUL-1987 US 071674 PI
 CORNELIUS MAXIN GOMAN
 PC C12N15/09, C12N5/10, C12N15/00, C12N5/00 CC
 FH key Location/Qualifiers
 FT source 1..773
 FEATURES
 source Location/Qualifiers
 1..777
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 188 a 205 c 190 g 194 t

ORIGIN

Query Match 46.1%; Score 256; DB 6; Length 777;
 Best Local Similarity 97.8%; Pred. No. 7e-41;
 Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 AGTATTATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCG 61
 DB 31 AGTATTATTAATGATCAATTAACGGGGTCATTAGTTCATAGCCCATATATGAGTTCCG 90

QY 62 GTTACATTAATGAGTAAATTTGGCCGCGCTGACGCCACCCAGACCCCGCCATTG 121
 DB 91 GTTACATTAATGAGTAAATTTGGCCGCGCTGACGCCACCCAGACCCCGCCATTG 150

QY 122 AGTCATTAATGACGTAAGTTCCTCCATAGTAACGCCAATAGGACTTTCATTGAGCTCA 181
 DB 151 AGTCATTAATGACGTAAGTTCCTCCATAGTAACGCCAATAGGACTTTCATTGAGCTCA 210

QY 182 TGGGTGAGATTAATGAGTAACTGCCA-TTGGCAGTACATCAAGTATCATATGCCA 240
 DB 211 TGGGTGAGATTAATGAGTAACTGCCA-TTGGCAGTACATCAAGTATCATATGCCA 270

QY 241 AGTACGCCCCCTATGAGTCAATGAGCGTAATG 276
 DB 271 AGTACGCCCCCTATGAGTCAATGAGCGTAATG 306

RESULT 10
 I05430
 LOCUS I05430 777 bp DNA linear PAT 02-DEC-1994
 DEFINITION Sequence 16 from Patent EP 0260148.
 ACCESSION I05430
 VERSION I05430.1 GI:591075
 KEYWORDS
 SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 777)
AUTHORS Gorman,C.M.
TITLE Improved recombinant expression method, vector and transformed cells
JOURNAL Patent: EP 0260148-A2 16 16-MAR-1988;
FEATURES location/Qualifiers
source 1..777
BASE COUNT 188 a 205 c 190 g 194 t
ORIGIN

Query Match 46.1%; Score 256; DB 6; Length 777;
Best Local Similarity 97.8%; Pred. No. 7e-41;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Db 2 AGTATTATATAGTATCAATTAACGGGGTCAATTAAGTTCATATATGAGTTCCGC 61
Db 31 AGTATTATATAGTATCAATTAACGGGGTCAATTAAGTTCATATATGAGTTCCGC 90
Qy 62 GTTACATTAATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 121
Db 91 GTTACATTAATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 150
Qy 122 AGTCAATTAATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 181
Db 151 AGTCAATTAATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 210
Qy 182 TGGGTGAGTATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 240
Db 211 TGGGTGAGTATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 270
Qy 241 AGTACGGCCCTATTAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 276
Db 271 AGTACGGCCCTATTAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 306

RESULT 11
LOCUS 108105
DEFINITION Sequence 3 from Patent EP 0309237.
ACCESSION 108105
VERSION 108105.1 GI:589184
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 777)
AUTHORS Gorman,C.M.
TITLE A transient expression system for producing recombinant protein
JOURNAL Patent: EP 0309237-A1 3 29-MAR-1989;
FEATURES location/Qualifiers
source 1..777
BASE COUNT 188 a 205 c 190 g 194 t
ORIGIN

Query Match 46.1%; Score 256; DB 6; Length 777;
Best Local Similarity 97.8%; Pred. No. 7e-41;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Db 2 AGTATTATATAGTATCAATTAACGGGGTCAATTAAGTTCATATATGAGTTCCGC 61
Db 31 AGTATTATATAGTATCAATTAACGGGGTCAATTAAGTTCATATATGAGTTCCGC 90
Qy 62 GTTACATTAATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 121
Db 91 GTTACATTAATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 150
Qy 122 AGTCAATTAATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 181
Db 151 AGTCAATTAATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 210

Qy 182 TGGGTGAGTATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 240
Db 211 TGGGTGAGTATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 270
Qy 241 AGTACGGCCCTATTAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 276
Db 271 AGTACGGCCCTATTAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 306

RESULT 12
LOCUS BD000143
DEFINITION Vector having stabilized sequence and eucaryotic host cell.
ACCESSION BD000143
VERSION BD000143.1 GI:18623222
KEYWORDS JP 2000308497-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 919)
AUTHORS Gorman,C.M.
TITLE Vector having stabilized sequence and eucaryotic host cell
JOURNAL Patent: JP 2000308497-A 1 07-NOV-2000;
COMMENT GENETIC INC
OS Unidentified
PN JP 2000308497-A/1
PD 07-NOV-2000
PF 17-APR-2000 JP 2000115248
PR 12-SEP-1986 US 907185,09-JUL-1987 US 071674 PI
CORNELIA MAXIN GORMAN
PC C12N15/09,C12N5/10,C12N15/00,C12N5/00
CC
FH key
FT source
FT 1..919
FEATURES location/Qualifiers
source 1..919
BASE COUNT 219 a 245 c 222 g 233 t
ORIGIN

Query Match 46.1%; Score 256; DB 6; Length 919;
Best Local Similarity 97.8%; Pred. No. 7e-41;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 2 AGTATTATATAGTATCAATTAACGGGGTCAATTAAGTTCATATATGAGTTCCGC 61
Db 31 AGTATTATATAGTATCAATTAACGGGGTCAATTAAGTTCATATATGAGTTCCGC 90
Qy 62 GTTACATTAATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 121
Db 91 GTTACATTAATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 150
Qy 122 AGTCAATTAATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 181
Db 151 AGTCAATTAATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 210
Qy 182 TGGGTGAGTATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 240
Db 211 TGGGTGAGTATTAAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 270
Qy 241 AGTACGGCCCTATTAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 276
Db 271 AGTACGGCCCTATTAGTATGAGTTCCGCAGTTCATATATGAGTTCCGC 306

RESULT 13
LOCUS 105393
DEFINITION Sequence 14 from Patent EP 0260148.
ACCESSION 105393

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VERSION      105393.1  GI:591073
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 919)
AUTHORS     Gorman,C.M.
TITLE       Improved recombinant expression method, vector and transformed
            cells
JOURNAL     Patent: EP 0260148-A2 14 16-MAR-1988;
FEATURES
            Location/Qualifiers
            source          1..919
BASE COUNT   219 a 245 c 222 g 233 t
ORIGIN
Query Match          46.1%; Score 256; DB 6; Length 919;
Best Local Similarity 97.8%; Pred. No. 7e-41;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY      2 AGTTATTAAATGATCAATTAAGCGGCTCATTTAGTCAAGCCCATATATGAGATTCCGC 61
DB      31 AGTTATTAAATGATCAATTAAGCGGCTCATTTAGTCAAGCCCATATATGAGATTCCGC 90

QY      62 GTTACATAACTTACGTAATTTGGCCCGGCTGACCGCCCAAGACCCCGCCCATTTG 121
DB      91 GTTACATAACTTACGTAATTTGGCCCGGCTGACCGCCCAAGACCCCGCCCATTTG 150

QY      122 ACGTCATAAATGACGTATGTTCCCATAGTAAGCCCATATGAGACTTTCATGACGTCAA 181
DB      151 ACGTCATAAATGACGTATGTTCCCATAGTAAGCCCATATGAGACTTTCATGACGTCAA 210

QY      182 TGGGTGAGATTTTACGTAATTTGCGCACTTGGCAGTACATCAAGTATCATATGCCA 240
DB      211 TGGGTGAGATTTTACGTAATTTGCGCACTTGGCAGTACATCAAGTATCATATGCCA 270

QY      241 AGTACGCCCCCTATTGACGTCAATGACGTAATATGG 276
DB      271 AGTACGCCCCCTATTGACGTCAATGACGTAATATGG 306

RESULT 14
LOCUS       108103          919 bp      DNA      linear      PAT 02-DEC-1994
DEFINITION  Sequence 1 from Patent EP 0309237.
ACCESSION   108103
VERSION     108103.1  GI:589182
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 919)
AUTHORS     Gorman,C.M.
TITLE       A transient expression system for producing recombinant protein
JOURNAL     Patent: EP 0309237-A1 1 29-MAR-1989;
FEATURES
            Location/Qualifiers
            source          1..919
            /organism="unknown"
BASE COUNT   219 a 245 c 222 g 233 t
ORIGIN
Query Match          46.1%; Score 256; DB 6; Length 919;
Best Local Similarity 97.8%; Pred. No. 7e-41;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY      2 AGTTATTAAATGATCAATTAAGCGGCTCATTTAGTCAAGCCCATATATGAGATTCCGC 61
DB      31 AGTTATTAAATGATCAATTAAGCGGCTCATTTAGTCAAGCCCATATATGAGATTCCGC 90

QY      62 GTTACATAACTTACGTAATTTGGCCCGGCTGACCGCCCAAGACCCCGCCCATTTG 121
DB      91 GTTACATAACTTACGTAATTTGGCCCGGCTGACCGCCCAAGACCCCGCCCATTTG 150

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QY      122 ACGTCATAAATGACGTATGTTCCCATAGTAAGCCCATATGAGACTTTCATGACGTCAA 181
DB      151 ACGTCATAAATGACGTATGTTCCCATAGTAAGCCCATATGAGACTTTCATGACGTCAA 210

QY      182 TGGGTGAGATTTTACGTAATTTGCGCACTTGGCAGTACATCAAGTATCATATGCCA 240
DB      211 TGGGTGAGATTTTACGTAATTTGCGCACTTGGCAGTACATCAAGTATCATATGCCA 270

QY      241 AGTACGCCCCCTATTGACGTCAATGACGTAATATGG 276
DB      271 AGTACGCCCCCTATTGACGTCAATGACGTAATATGG 306

RESULT 15
LOCUS       AR028792          930 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5858784.
ACCESSION   AR028792
VERSION     AR028792.1  GI:5940765
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 930)
AUTHORS     Debs,R.James. and Zhu,N.
TITLE       Expression of cloned genes in the lung by aerosol- and
            liposome-based delivery
JOURNAL     Patent: US 5858784-A 2 12-JAN-1999;
FEATURES
            Location/Qualifiers
            source          1..930
            /organism="unknown"
BASE COUNT   233 a 228 c 211 g 258 t
ORIGIN
Query Match          46.1%; Score 256; DB 6; Length 930;
Best Local Similarity 97.8%; Pred. No. 7e-41;
Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY      2 AGTTATTAAATGATCAATTAAGCGGCTCATTTAGTCAAGCCCATATATGAGATTCCGC 61
DB      157 AGTTATTAAATGATCAATTAAGCGGCTCATTTAGTCAAGCCCATATATGAGATTCCGC 216

QY      62 GTTACATAACTTACGTAATTTGGCCCGGCTGACCGCCCAAGACCCCGCCCATTTG 121
DB      217 GTTACATAACTTACGTAATTTGGCCCGGCTGACCGCCCAAGACCCCGCCCATTTG 276

QY      122 ACGTCATAAATGACGTATGTTCCCATAGTAAGCCCATATGAGACTTTCATGACGTCAA 181
DB      277 ACGTCATAAATGACGTATGTTCCCATAGTAAGCCCATATGAGACTTTCATGACGTCAA 336

QY      182 TGGGTGAGATTTTACGTAATTTGCGCACTTGGCAGTACATCAAGTATCATATGCCA 240
DB      337 TGGGTGAGATTTTACGTAATTTGCGCACTTGGCAGTACATCAAGTATCATATGCCA 396

QY      241 AGTACGCCCCCTATTGACGTCAATGACGTAATATGG 276
DB      397 AGTACGCCCCCTATTGACGTCAATGACGTAATATGG 432

Search completed: December 15, 2002, 06:47:24
Job time : 3138 secs

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FF	22-JUN-1999;	99JP-0174804.
PR	22-JUN-1999;	99JP-0174804.
XX		
XX	(JAPG)	NIPON ZEON KK.
DR	WPI, 2001-285232/30.	
XX		
PT	New DNA molecule for use as a promoter for preparing a recombinant	
PT	containing the DNA which is used for preparing a vaccine -	
PS	Example 1; Page 11; 15pp; Japanese.	
XX		
CC	The invention relates to a 5' and a 3' fragment of the chicken beta-actin	
CC	promoter (AA884452 and AA884453, respectively), which exhibit promoter	
CC	activity. The chicken beta-actin promoter fragments may be used to drive	
CC	expression of a heterologous gene in a recombinant vector used as the	
CC	active component of a genetic vaccine. The present invention represents	
CC	a chimeric promoter, Pec, which was constructed in an exemplification of	
CC	the invention. The Pec promoter comprises a cytomagalovirus (CMV)	
CC	immediate-early (IE) promoter fragment, and a 5' fragment of the chicken	
CC	beta-actin promoter.	
XX		
SO	Sequence 561 BP; 109 A; 156 C; 191 G; 105 T; 0 other;	
Query Match	95.5%; Score 530; DB 22; Length 561;	
Best Local Similarity	99.5%; Pred. No. 3.2e-99;	
Matches 553; Conservative 0; Mismatches 0; Indels 3; Gaps 2;		
QY	2 AGTTTAAATGATCAATTAACGGGGTCAATAGTTCATAGCCCATATATGAGTTCCGC	61
Db	1 AGTTTAAATGATCAATTAACGGGGTCAATAGTTCATAGCCCATATATGAGTTCCGC	60
QY	62 GTTACATACTTACCGGTAATTGCGCCGCGCTGACCGCCACAGACCCCGCCCATTTG	121
Db	61 GTTACATACTTACCGGTAATTGCGCCGCGCTGACCGCCACAGACCCCGCCCATTTG	119
QY	122 ACGTCAATTAATGAGTATGTTCCCATTAAGTACGCCAATATAGGACCTTCCATTGAGCTCA	181
Db	120 ACGTCAATTAATGAGTATGTTCCCATTAAGTACGCCAATATAGGACCTTCCATTGAGCTCA	179
QY	182 TGGGGGAGTATTTACGGTAAACATGCCCATTTGGCATATCAAGTATCATATATGCCAA	241
Db	180 TGGGGGAGTATTTACGGTAAACATGCCCATTTGGCATATCAAGTATCATATATGCCAA	239
QY	242 GTACGCCCCCTTATACGTCATATGACGGTAATGAGTACGATTTTGTGCAGCGATGGG	301
Db	240 GTACGCCCCCTTATACGTCATATGACGGTAATGAGTACGATTTTGTGCAGCGATGGG	299
QY	302 GGC--GGGGGGGGGGGGCGCGCCAGCGGGGGGGGGGGGGGCGAGGGGGGGGGG	359
Db	300 GGC--GGGGGGGGGGGGCGCGCCAGCGGGGGGGGGGGGGGCGAGGGGGGGGGG	359
QY	360 CGAGCGCGGAGAGTCCGCGCGGACGTCATCAAGGCGGGCGCGTCCGAAAGTTCTTTTA	419
Db	360 CGAGCGCGGAGAGTCCGCGCGGACGTCATCAAGGCGGGCGCGTCCGAAAGTTCTTTTA	419
QY	420 TGGCAGAGGGGGGGGGGGCGCGCCCTTATATAAAGGAGAGCGGCGGGGGGAGATGG	479
Db	420 TGGCAGAGGGGGGGGGGGCGCGCCCTTATATAAAGGAGAGCGGCGGGGGGAGATGG	479
QY	480 CTGCGCGCTGCTTGGCCCGCGTCCGCGCGCGCGCTGCGCGCGCGCGCGCGCGG	539
Db	480 CTGCGCGCTGCTTGGCCCGCGTCCGCGCGCGCGCTGCGCGCGCGCGCGCGCGG	539
QY	540 TCTGACTGACCGCGTTC	555
Db	540 TCTGACTGACCGCGTTC	555

RESULT 2

AAZ45930

ID: AAZ45930 standard; DNA: 6714 BP.

XX	AA245930;
AC	
DX	25-APR-2000 (first entry)
DT	
XX	
DE	Nucleotide sequence of the vector pA3CB-AT.
KW	Viral vector: pA3CB-AT; alpha-1-antitrypsin; gene therapy; diabetes;
KM	alpha-1-antitrypsin deficiency; haemophilia; neurological disorder;
RN	adenosine deaminase deficiency; autoimmune disease; interleukin-2;
KX	immunodeficiency disease; infection; cytokine; circular; cancer; ss.
OS	Synthetic.
OS	Adeno associated virus.
OS	Homo sapiens.
OS	Calliflower mosaic virus.
XX	Gallus sp.
PX	MO9955564-AI.
PD	04-NOV-1999.
XX	
PF	23-APR-1999; 99WO-US08921.
XX	
PR	24-APR-1998; 98US-0083025.
XX	
PA	(UYFL.) UNIV FLORIDA.
PI	Floette TR, Song S, Byrnes BJ, Morgan M;
XX	
DR	WPI: 2000-147020/13.
XX	
PT	Recombinant viral vector useful in the gene therapy of
XX	alpha-1-antitrypsin deficiency and also in hemophilia and diabetes -
PS	Claim 32; Fig 20A-C; 85pp; English.
XX	
CC	The present sequence represents a recombinant viral vector, designated
CC	pA3CB-AT, which encodes human alpha-1-antitrypsin protein, and which
CC	contains the CMV enhancer, and chicken beta-actin promoter sequences.
CC	The vector is exemplary of the vectors of the invention which comprise
CC	a polynucleotide encoding a protein, and are used for gene therapy to
CC	correct genetic disorders related to expression of a protein of interest.
CC	The vectors of the invention are based on Adeno associated virus (AAV).
CC	The vectors comprise AAV inverted terminal repeats and constitutive or
CC	regulatable promoters for driving high levels of gene expression.
CC	Vectors encoding alpha-1-antitrypsin protein or a biologically active
CC	fragment or variant are administered to mammalian cells (preferably
CC	myofibers, myoblasts, hepatocytes or lung cells) for treating
CC	alpha-1-antitrypsin deficiency or ameliorating a condition resulting
CC	from a defective protein. The vectors can also be useful for genetic
CC	therapy of other conditions such as hemophilia, adenosine deaminase
CC	deficiency, diabetes, cancer, autoimmune diseases, neurological
CC	disorders, immunodeficiency diseases and bacterial or viral infections
CC	by the infusion of protein or a cytokine such as Interleukin-2.
XX	
SQ	Sequence 6714 BP; 1452 A; 1821 C; 1886 G; 1555 T; 0 other;
	Query Match 58.6%; Score 325; DB 21; Length 6714;
	Best Local Similarity 74.9%; Pred. No. 2e-57; Indels 172; Gaps
	Matches 543; Conservative 0; Mismatches 10;
OY	2 AGTTATTATAATGTAATTCAGGGGTCATTAGTTCATAGGCCCATATATGAGGTCCGC 61
DB	323 AGTTATTATAATGTAATTCATTCAGGGGTCATTAGTTCATAGGCCCATATATGAGGTCCGC 382
OY	62 GTTACATAACTTAGGTAATTTGGCCCGCGCTGACGCGCCCAAGACCCTCCGCCATTG 121
DB	383 GTTACATAACTTAGGTAATTTGGCCCGCGCTGACGCGCCCAAGACCCTCCGCCATTG 442
OY	122 AGCTCAATTAATGACGTATGTTCCCATAGTAAGAACCCAAATGGAGACTTTCATGAGCTCAA 181
DB	443 AGCTCAATTAATGACGTATGTTCCCATAGTAAGAACCCAAATGGAGACTTTCATGAGCTCAA 502

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OY 182 TGGGTGAGATATTACGGTAAACCTGCCA-TTGGCAGTACATCAAGTGATATATGCCA 240
DB 503 TGGGTGAGATATTACGGTAAACCTGCCA-TTGGCAGTACATCAAGTGATATATGCCA 562
OY 241 AGTACGGCCCTATTGACGTCAATGACGTAATAG----- 276
DB 563 AGTCCGCCCTATTGACGTCAATGACGTAATAGGCCCTGGCATTATGCCAGTAC 622
OY 277 ----- 276
DB 623 ATGACCTTACGGACTTCTACTTGCGATACATCTACATCTATTCCTATTAC 682
OY 277 ----- 276
DB 683 ATGTCGAGTATGAGCCCACTTCGCTTCACTCCCATCTCCCTCCCTCCCAACC 742
OY 277 -----ATGCACTATTATTGTCAGCATGGGGC---GGGGGG 310
DB 743 CCAATTTTGTATTATTATTATTATTATTATTATTGTGTCAGCATGGGGC 802
OY 311 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 370
DB 803 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 862
OY 371 GGTGCGGCGGAGCCATCAGAGCGCGCTCCGAAAGTTTCTTTTATGCGAGGCGG 430
DB 863 GGTGCGGCGGAGCCATCAGAGCGCGCTCCGAAAGTTTCTTTTATGCGAGGCGG 922
OY 431 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 489
DB 923 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 982
OY 490 CCTTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 549
DB 983 CCTTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1042
OY 550 CGCGT 554
DB 1043 CGCGT 1047

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RESULT 3

AAZ45934
ID AAZ45934 standard; DNA; 6924 BP.

AC AAZ45934:

DT 25-APR-2000 (first entry)

DE Nucleotide sequence of the vector p43msENCB-AT.

KM Viral vector; p43msENCB-AT; alpha-1-antitrypsin; gene therapy; diabetes;

KM alpha-1-antitrypsin deficiency; haemophilia; neurological disorder;

KM adenosine deaminase deficiency; autoimmune disease; interleukin-2;

KM immunodeficiency disease; infection; cytokine; circular; cancer; ss.

OS Synthetic.

OS Adeno associated virus.

OS Homo sapiens.

OS Cauliflower mosaic virus.

OS Gallus sp.

XX W09955564-A1.

XX 04-NOV-1999.

XX 23-APR-1999; 99MO-US08921.

XX 24-APR-1998; 98US-0083025.

XX (UWFL) UNIV FLORIDA.

PI Plotte TR, Song S, Byrnes BJ, Morgan M;
XX WPI; 2000-147020/13.
XX
PT Recombinant viral vector useful in the gene therapy of
PT alpha-1-antitrypsin deficiency and also in hemophilia and diabetes -
XX
PS Claim 32; Fig 24A-C; 85pp; English.
XX
CC The present sequence represents a recombinant viral vector, designated
CC p43msENCB-AT, which encodes human alpha-1-antitrypsin protein, and
CC which contains the CMV enhancer, and chicken beta actin promoter
CC sequences, and has an enhancer sequence upstream of the CMV promoter.
CC The vector is exemplary of the vectors of the invention which comprise
CC a polynucleotide encoding a protein, and are used for gene therapy to
CC correct genetic disorders related to expression of a protein of interest.
CC The vectors of the invention are based on Adeno associated virus (AAV).
CC The vectors comprise AAV inverted terminal repeats and constitutive or
CC regulatable promoters for driving high levels of gene expression.
CC Vectors encoding alpha-1-antitrypsin protein or a biologically active
CC fragment or variant are administered to mammalian cells (preferably
CC myofibers, myoblasts, hepatocytes or lung cells) for treating
CC alpha-1-antitrypsin deficiency or ameliorating a condition resulting
CC from a defective protein. The vectors can also be useful for genetic
CC therapy of other conditions such as hemophilia, adenosine deaminase
CC deficiency, diabetes, cancer, autoimmune diseases, neurological
CC disorders, immunodeficiency diseases and bacterial or viral infections
CC by the infusion of protein or a cytokine such as interleukin-2.
XX
SQ Sequence 6924 BP; 1504 A; 1866 C; 1951 G; 1603 T; 0 other;

Query Match 58.6%; Score 325; DB 21; Length 6924;
Best Local Similarity 74.9%; Pred. No. 2e-57;
Matches 543; Conservative 0; Mismatches 10; Indels 172; Gaps 4;

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OY 2 AGTATTAAATAGTAAATACATTTACGGGGTCTTATGTTTCATATGCCATATATGAGTCCG 61
DB 533 AGTATTAAATAGTAAATACATTTACGGGGTCTTATGTTTCATATGCCATATATGAGTCCG 592
OY 62 GTTACATTAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAG 121
DB 593 GTTACATTAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAG 652
OY 122 AGTCAATATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAG 181
DB 653 AGTCAATATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAG 712
OY 182 TGGGTGAGATATTACGGTAAACCTGCCA-TTGGCAGTACATCAAGTGATATATGCCA 240
DB 713 TGGGTGAGATATTACGGTAAACCTGCCA-TTGGCAGTACATCAAGTGATATATGCCA 772
OY 241 AGTACGGCCCTATTGACGTCAATGACGTAATAG----- 276
DB 773 AGTCCGCCCTATTGACGTCAATGACGTAATAGGCCCTGGCATTATGCCAGTAC 832
OY 277 ----- 276
DB 833 ATGACCTTACGGACTTCTACTTGCGATACATCTACATCTATTCCTATTAC 892
OY 277 ----- 276
DB 893 ATGTCGAGTATGAGCCCACTTCGCTTCACTCCCATCTCCCTCCCTCCCAACC 952
OY 277 -----ATGCACTATTATTGTCAGCATGGGGC---GGGGGG 310
DB 953 CCAATTTTGTATTATTATTATTATTATTATTATTATTGTGTCAGCATGGGGC 1012
OY 311 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 370
DB 1013 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1072
OY 371 GGTGCGGCGGAGCCATCAGAGCGCGCTCCGAAAGTTTCTTTTATGCGAGGCGG 430

```


XX
PA (DELT-) DELTAGEN INC.

PI Slebel C, Brennan TJ;

DR WPI; 2002-383132/41.

PT Novel targeting vector modifying target gene, has first and second
PT sequences homologous to target gene portions, a selectable marker
PT cassette and regulator, useful for producing animals with targeted gene
PT modifications -

PS Example 1; Flg 14A-B; 43pp; English.

CC The invention describes a targeting vector (positive selection vector)
CC (I) capable of modifying a target gene. (I) comprises two sequences
CC (S1 and S2) homologous to a portion or region of a target gene, a
CC selectable marker cassette and a regulator. (I) is useful for producing
CC cells comprising a modification of the target gene which involves
CC introducing (I) into cells capable of homologous recombination, selecting
CC for cells expressing the selectable marker and identifying cells
CC containing the modification of the target gene. Use of (I) for enriching
CC cells comprising disruption or modification of target gene enhances
CC recovery of cells having targeting vector integrated via homologous
CC recombination into the genomes of the cells. (I) is capable of modifying
CC target gene in a cell with high efficiency and specificity. Use of (I)
CC provides a faster and more efficient means for isolating and selecting
CC cells comprising target gene modification. Also use of (I) provides an
CC increase over previous technologies in both the speed and frequency at
CC which homologous recombination events can be recovered. (I) is also
CC useful for creation of transgenic animals containing targeted gene
CC modifications. This sequence represents the positive selection vector
CC construct c3408.

SQ Sequence. 5759 BP; 1274 A; 1526 C; 1658 G; 1301 T; 0 other;

Query Match	Score	DB	Length
Best Local Similarity	55.7%;	309.4;	5759;
	74.6%;	Pred. No. 2.9e-54;	

Matches 539; Conservative 0; Mismatches 11; Indels 173; Gaps 5;

[illegible]

Db 539 GGGGGCGCGCCGAGCGGGCGGGCGCGCGCGCGCGCGCGCGAGCGCGAGAG 598

372 GTGCGGCGCAGCCAATCAGAGCGCGCGCTCCGAAATTCTTTATGCGGAGCGGC 431

Db 599 GTGCGGCGGCGCAATCAGAGCGGCGCTCCGAACTTCTTTATGGCGAGGCGC 658

QY 432 GCGGCGGCCCTATAAAGCGAGCGCGCGGAGTCGCTGCGCGTGC 491

Db 659 GCGGCGGCGCCCTATAAAAGCGAAGCGCGCGCGGAGTCGCT--GCGTTGCC 716

492 TTCGCCCCGTCGCCGCCGCGCTCGGCCGCCGCCGCCGCTTGACTGACCG 551

Db 717 TTCGCCCCGTCGCCGCTCCG-CGCCGCTCGCGCCGCCGCCGCCGCCGCTCTGACTGACCG 775

QY 552 CGT 554

Db 776 CGT 778

RESULT 10

ID ABK49520 standard; DNA; 6148 BP.

AC ABK49520;

DT 15-JUL-2002 (first entry)

DE Positive selection vector construct c3406.

KW Transgenic animal; targeting vector; positive selection vector;

KW C3406; ds.

OS Synthetic.

PN WO200222283

PD 21-MAR-2002.

PF 17-SEP-2001; 2001WO-US28892.

PR 15-SEP-2000; 2000US-232957P.

PA (DELT-) DELTAGEN INC.

PI Siebel C, Brennan TJ

DR WPI; 2002-383132/41

PT Novel targeting vect

PT cassette and regulator, useful for producing animals with targeted gene modifications.

XX
XX
C1313 22. E12 51. 4300. E0714b

CC The invention describes a targeting vector (positive selection vector)
CC (1) capable of modifying a target gene. (1) comprises two sequences
CC (S1 and S2) homologous to a portion or region of a target gene, a
CC selectable marker cassette and a regulator. (1) is useful for producing
CC cells comprising a modification of the target gene which involves
CC introducing (1) into cells capable of homologous recombination, selecting
CC for cells expressing the selectable marker and identifying cells
CC containing the modification of the target gene. Use of (1) for enriching
CC cells comprising disruption or modification of target gene enhances
CC recovery of cells having targeting vector integrated via homologous
CC recombination into the genomes of the cells. (1) is capable of modifying
CC target gene in a cell with high efficiency and specificity. Use of (1)
CC provides a faster and more efficient means for isolating and selecting
CC cells comprising target gene modification. Also use of (1) provides an
CC increase over previous technologies in both the speed and frequency at
CC which homologous recombination events can be recovered. (1) is also

CC useful for creation of transgenic animals containing targeted gene
 CC modifications. This sequence represents the positive selection vector
 CC construct c3406.

XX Sequence 6148 BP; 1354 A; 1593 C; 1770 G; 1431 T; 0 other;

Query Match 55.7%; Score 309.4; DB 24; Length 6148;
 Best Local Similarity 74.6%; Pred. No. 2.9e-54;
 Matches 539; Conservative 0; Mismatches 11; Indels 173; Gaps 5;

```

OY 2 AGTATTAATTAATCAATTAAGGAGTCTTGTTCATGACCCATATAGAGTCCGC 61
DB 2515 AGTATTAATTAATCAATTAAGGAGTCTTGTTCATGACCCATATAGAGTCCGC 2574
OY 62 GTTACATTAATTAAGTAAATGCGCGCGGTGACCGCCCAAGACCCGCCCATTTG 121
DB 2575 GTTACATTAATTAAGTAAATGCGCGCGGTGACCGCCCAAGACCCGCCCATTTG 2634
OY 122 ACCTCAATAATGAGTATGTTCCCATATGACGCCAATAGGAGCTTTCATGACGTCA 181
DB 2635 ACCTCAATAATGAGTATGTTCCCATATGACGCCAATAGGAGCTTTCATGACGTCA 2694
OY 182 TGGGTGAGTATTAAGTAAATGCGCGCGGTGACCGCCCAAGACCCGCCCATTTG 240
DB 2695 TGGGTGAGTATTAAGTAAATGCGCGCGGTGACCGCCCAAGACCCGCCCATTTG 2754
OY 241 AGTACGCCCCCTATGACGTCAATGAGGTAATG----- 276
DB 2755 AGTACGCCCCCTATGACGTCAATGAGGTAATG----- 2814
OY 277 ----- 276
DB 2815 ATGACCTTAAGGAGCTTCTCTACTTGACATCATGATTAATGATCGCATTTAC 2874
OY 277 ----- 276
DB 2875 ATGCTTCGAGGTGAGCCCGACGTTCTGCTTCACTCTCCCATCTCCCGCCACCC 2934
OY 277 ----- 276
DB 2935 CCAATTTTGTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2994
OY 312 GGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 371
DB 2995 GGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3054
OY 372 GTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 431
DB 3055 GTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3114
OY 432 GGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 491
DB 3115 GGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3172
OY 492 TTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 551
DB 3173 TTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3232
OY 552 CGT 554
DB 3232 CGT 3234

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RESULT 11

ALA3173
 ID ALA3173 standard; cDNA; 6256 BP.

XX ALA3173;

XX 16-AUG-2002 (first entry)

XX PCAGGS-hSEPOR2 rat Iggl Fc cDNA sequence.

XX

KM Rat; ss; expression product activity regulation;
 KW PCAGGS-hSEPOR2 rat Iggl Fc.
 XX
 OS Chimeric - Rattus sp.
 OS Chimeric - Unidentified.

XX WO200241922-A1.

XX 30-MAY-2002.

XX 28-SEP-2001; 2001MO-JP08575.

XX 24-NOV-2000; 2000JP-0358389.

XX (CHUS) CHUGAI SEIYAKU KK.

XX (MARU) MARIYAMA H.

XX Maruyama H, Miyazaki J, Sugawa M, Higuchi M;

XX WPI; 2002-471702/50.

PT Regulating activity of expression product of gene transferred into
 PT living body by coexistence of interfering substance e.g. expression
 PT product receptor, given through skin to express and reduce excessive
 PT activity

PS Example 4; Page 39-43; 49pp; Japanese.

CC The invention comprises a method for regulating the activity of an
 CC expression product of a gene transferred into a living body. The method
 CC involves the coexistence of a protein interfering with the activity of
 CC the expression product. The method of the invention is useful for
 CC regulating the activity of an expression product. The present chimeric
 CC DNA sequence was used in an example of the invention.

XX Sequence 6256 BP; 1314 A; 1713 C; 1758 G; 1471 T; 0 other;

Query Match 55.7%; Score 309.4; DB 24; Length 6256;
 Best Local Similarity 74.6%; Pred. No. 3e-54;
 Matches 539; Conservative 0; Mismatches 11; Indels 173; Gaps 5;

```

OY 2 AGTATTAATTAATCAATTAAGGAGTCTTGTTCATGACCCATATAGAGTCCGC 61
DB 21 AGTATTAATTAATCAATTAAGGAGTCTTGTTCATGACCCATATAGAGTCCGC 80
OY 62 GTTACATTAATTAAGTAAATGCGCGCGGTGACCGCCCAAGACCCGCCCATTTG 121
DB 81 GTTACATTAATTAAGTAAATGCGCGCGGTGACCGCCCAAGACCCGCCCATTTG 140
OY 122 ACCTCAATAATGAGTATGTTCCCATATGACGCCAATAGGAGCTTTCATGACGTCA 181
DB 141 ACCTCAATAATGAGTATGTTCCCATATGACGCCAATAGGAGCTTTCATGACGTCA 200
OY 182 TGGGTGAGTATTAAGTAAATGCGCGCGGTGACCGCCCAAGACCCGCCCATTTG 240
DB 201 TGGGTGAGTATTAAGTAAATGCGCGCGGTGACCGCCCAAGACCCGCCCATTTG 260
OY 241 AGTACGCCCCCTATGACGTCAATGAGGTAATG----- 276
DB 261 AGTACGCCCCCTATGACGTCAATGAGGTAATG----- 320
OY 277 ----- 276
DB 321 ATGACCTTAAGGAGCTTCTCTACTTGACATCATGATTAATGATCGCATTTAC 380
OY 277 ----- 276
DB 381 ATGAGTGAGGTGAGCCCGACGTTCTGCTTCACTCTCCCATCTCCCGCCCTCCAC 440
OY 277 ----- 276
DB 441 CCAATTTTGTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 500

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QY	312	GGGGGGGGCCAGAGCGGGGGCGGGGGCGAGAGGGGGCGAGCGCGAGAG	371
Db	501	GGGGGGCGCCCGCAGCGGGGGGGGGCGGGCGAGGGGGCGAGGGCGAGAG	560
QY	372	GTGGGGGGCGAGCCAAATCAGAGCGGGCGCGCTCCGAAAGTTTCTTTATGSGCAGCGCGC	431
Db	561	GTGGGGGGCGAGCCAAATCAGAGCGGGCGCGCTCCGAAAGTTTCTTTATGSGCAGCGCGC	620
QY	432	GGCGGGGGCGGCGCTATATAAAGGGAAGCGCGGGGGCGGAGTGCCTGCGCGCTGCC	491
Db	621	GGCGGGGGCGGCGCTATATAAAGGGAAGCGCGGGGGCGGAGTGCCT--GGCTTGCC	678
QY	492	TTTCGGCGCGTCCCGCGCTCGCGCGCGCGCTCGCGCGCGCGCGCGCGCTGTGACTGACCG	551
Db	679	TTTCGGCGCGTCCCGCGCTCGCGCGCGCGCTCGCGCGCGCGCGCGCGCTGTGACTGACCG	737
QY	552	CGT	554
Db	738	CGT	740

RESULT 12
AAF84456
ID AAF84456 standard; DNA; 599 BP.
VY

AC AAF84456;

DT 25-JUN-2001 (first entry)

DE Cytomegalovirus (CMV) immediate-early (IE) promoter enhancer.

KW Cytomegalovirus; CMV; immediate-early; IE promoter enhancer;

KW recombinant vector; genetic vaccine; gene therapy; ds

OS Human cytomegalovirus

PN JP2001.0000188-A
YY

09-JAN-2001.
PD
xy

PF 22-JUN-1999; 99JP-0174804.
VY

PR 22-JUN-1999; 99JP-0174804.

PA (JAPG) NIPPON ZEON KK.

DR WPI; 2001-285232/30.

PT New DNA molecule for use as a promoter for preparing a recombinant

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CC The invention relates to a 5' and a 3' fragment of the chicken beta-actin
CC promoter (AA844452 and AA844453, respectively), which exhibit promoter
CC activity. The chicken beta-actin promoter fragments may be used to drive
CC expression of a heterologous gene in a recombinant vector used as the
CC active component of a genetic vaccine. The present sequence represents
CC a cytomegalovirus (CMV) immediate-early (IE) promoter enhancer, a
CC portion of which was used in the construction of the chimeric Pec
CC promoter (AA844454) in an exemplification of the invention.

50 Sequence 599 BP; 152 A; 144 C; 144 G; 159 T; 0 other;

Query Match	46.38;	Score 257;	DB 22;	Length 599;
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Matches 271; Conservative 0; Mismatches 5; Indels 1; Gaps 1

Oy 1 GAGTTATTAAATGTATTCATTACGGGGCTATTGTTTCATAGCCCATATATGGAGTTCGC 600
|||||
Db 6 GAGTTATTAAATGTATTCATTACGGGGCTATTGTTTCATAGCCCATATATGGAGTTCGC 655

[illegible]

RESULT 13
AA15163/c
ID AA15163 standard; DNA; 589 BP.

AA15163

DT 22-APR-1999 (first entry)
 YY

Human cytomegalovirus promoter region.

KW apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy. cancer. cystic fibrosis.

KW non-small cell lung carcinoma; diabetes; arteriosclerosis;
KW Human cytomegalovirus promoter region; ss

Human automata] our rus
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PN W09856938-A1

XX.
PD : 17-DEC-1998

XX 10-JIN-1998: 98WO-ΠS11927

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PR 14-MAY-1998: 98TIS-0079030

PR 13-JUN-1997; 9705-0874807.
XX

PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX

PI Guevara JG, Hoogeveen RC, Moore JP;
XX

DR WPI; 1999-070331/06.
XX

PT Composition comprising nucleic acid bound to LDL or VLDL lipoprotein used for delivering nucleic acid to cells for gene therapy and

PT antisense treatment
XY

PS Example 4; Page 74; 293pp; English.

CC The present sequence represents the Human cytomegalovirus promoter
CC region. The compositions of the invention bind to this sequence.
CC The specification describes a composition that comprises low
CC density lipoprotein (LDL) and apolipoproteins for the binding and
CC in vivo transport of nucleic acids. The composition is used to deliver
CC nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing
CC a therapeutic polypeptide or antisense molecule (or ribozyme).
CC Specifically they are used for gene therapy of cancers (particularly
CC non-small cell lung carcinoma), diabetes, cystic fibrosis and
CC arteriosclerosis.

SQ Sequence 589 BP; 157 A; 140 C; 143 G; 149 T; 0 other;

Query Match	46.18;	Score 256;	DB 20;	Length 589;
Post local classification	07.08;	Prod No 3	1043;	

Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1.

QY 2 AGTTATTAACTAGTAATCAATTACGGGTCATTAGTTCATAGCCCATATATGGAGTTCGC 61

DB 588 AGTATTAAATAGTAAATACGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 529
 QY 62 GTTACATTAATAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 121
 DB 528 GTTACATTAATAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 469
 QY 122 ACCTCAATTAATAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 181
 DB 468 ACCTCAATTAATAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 409
 QY 182 TGGGTGAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 240
 DB 408 TGGGTGAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 349
 QY 241 AGTACGCCCCCTATTGAGTCAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 276
 DB 348 AGTACGCCCCCTATTGAGTCAATGAGGAGTCAATGAGTTCCGC 313

RESULT 14

AAH24425 ID AAH24425 standard; DNA; 590 BP.

AAH24425; AC XX

02-AUG-2001 (first entry) DE XX

Cauliflower mosaic virus promoter. DE XX

Cauliflower mosaic virus; promoter; signal peptide; chloroplast; gene expression; protein production; human growth hormone; ds. KM XX

Cauliflower mosaic virus. OS XX

JP2000354490-A. PN XX

26-DEC-2000. PD XX

15-JUN-1999; 99JP-0168271. PF XX

15-JUN-1999; 99JP-0168271. PR XX

(TOYOTA) TOYOTA JIDOSHA KK. PA XX

WPI; 2001-275809/29. DR XX

New signal peptides useful for the preparation of human growth hormone and transformed chloroplast. PT XX

Example 1; Page 12; 15pp; Japanese. PS XX

The present sequence is provided in a specification relating to signal peptides for expression and secretion of a protein in chloroplast. The CC XX

Met-Ala-Ser-Lys-X₁-X₂-Ala-Ser-Gly. CC XX

n = an integer of 5-15; CC XX

The signal peptides are useful in the preparation of human growth hormone and transformed chloroplast. Signal peptides; DNA encoding the CC XX

cassettes, gene expression cassettes, recombinant vectors containing the CC XX

present sequence is a promoter which may be used in the invention. CC XX

Sequence 590 BP; 149 A; 143 C; 141 G; 157 T; 0 other; SQ

Query Match 46.1%; Score 256; DB 22; Length 590; Best Local Similarity 97.8%; Pred. No. 2.3e-43; Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

2 AGTATTAAATAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 61
 |||

DB 2 AGTATTAAATAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 61
 QY 62 GTTACATTAATAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 121
 DB 62 GTTACATTAATAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 121
 QY 122 ACCTCAATTAATAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 181
 DB 122 ACCTCAATTAATAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 181
 QY 182 TGGGTGAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 240
 DB 182 TGGGTGAGTAAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 241
 QY 241 AGTACGCCCCCTATTGAGTCAATGAGGAGTCAATGATTCATACCCCATATATGAGTTCCGC 276
 DB 242 AGTACGCCCCCTATTGAGTCAATGAGGAGTCAATGAGTTCCGC 277

RESULT 15

AA295643 ID AA295643 standard; DNA; 763 BP.

AA295643; AC XX

08-JUN-2000 (first entry) DE XX

Cytomegalovirus derived promoter sequence SEQ ID NO:1. DE XX

Cytomegalovirus; CMV; promoter; human growth hormone; PGH; ovine; KM XX

cardiac; thrombolytic; anti-inflammatory; gene therapy; KM XX

pulmonary embolus; myocardial infarction; lung disease; KM XX

adult respiratory distress syndrome; ds. KM XX

Human cytomegalovirus. OS XX

US6030638-A. PN XX

29-FEB-2000. PD XX

02-JUN-1995; 95US-0459493. PF XX

19-AUG-1991; 91US-0746941. PR XX

21-JUN-1993; 93US-0080221. PA XX

(UYVA-) UNIV VANDERBILT. PA XX

Meyrick B, Canonico A, Brigham K, Conary JT; PI XX

WPI; 2000-205193/18. PI XX

Increasing prostanoid production in vivo comprising delivering and PT XX

hyperexpressing a prostaglandin synthase gene in cells; useful for treating e.g. myocardial infarction and general lung disease - PT XX

Disclosure; Column 7-10; 11pp; English. PS XX

A method has been developed of increasing prostanoid production in vivo CC XX

comprising delivering and hyperexpressing a prostaglandin synthase gene CC XX

in cells. The method can be used for gene therapy. The method is useful CC XX

for the treatment of diseases such as pulmonary embolus, myocardial CC XX

infarction and general lung disease (e.g. adult respiratory distress CC XX

syndrome). Generally the present invention provides a plasmid comprising CC XX

a cytomegalovirus (CMV) derived promoter sequence driving the coding CC XX

region for ovine prostaglandin G/H synthase (PGH). In order to increase CC XX

the expression of the gene, the construct also contains a short CC XX

translation augmenting sequence and a portion of the 3' untranslated CC XX

region from the human growth hormone (hGH) gene. The present sequence CC XX

represents the CMV promoter sequence used in the exemplification of the CC XX

present invention. CC XX

Sequence 763 BP; 203 A; 174 C; 164 G; 222 T; 0 other; SQ

Query Match 46.1%; Score 256; DB 21; Length 763;
 Best Local Similarity 97.8%; Pred. No. 2.1e-43;
 Matches 270; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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OY 2 AGTTATTAATAGTATCAATTACGGGGTCATTAGTTCATAGCCCATATATGAGTCCGC 61
    |||||||
DB 180 AGTTATTAATAGTATCAATTACGGGGTCATTAGTTCATAGCCCATATATGAGTCCGC 239
    |||||||

OY 62 GTTACATAACTTACGTAATTTGGCCCGGCTGACGCCGACGCCGCCGCCATTG 121
    |||||||
DB 240 GTTACATAACTTACGTAATTTGGCCCGGCTGACGCCGACGCCGCCGCCATTG 299
    |||||||

OY 122 ACGTAATAATGACGTATGTTCCCATAGTAACGCCAATAGGACTTTCATTGACGTCAA 181
    |||||||
DB 300 ACGTAATAATGACGTATGTTCCCATAGTAACGCCAATAGGACTTTCATTGACGTCAA 359
    |||||||

OY 182 TGGGTGAGTATTTACGGTAACCTGCCA-TTGGCAGTACATCAAGTATCATATAGCCA 240
    |||||||
DB 360 TGGGTGAGTATTTACGGTAACCTGCCA-TTGGCAGTACATCAAGTATCATATAGCCA 419
    |||||||

OY 241 AGTACGCCCCCTATTGACGTCAATGACGGTAATGG 276
    |||||||
DB 420 AGTACGCCCCCTATTGACGTCAATGACGGTAATGG 455
    |||||||
    
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 Job time : 318 secs